

GenCore version 5.1.4.p5_4578
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OM protein - protein search, using sw model

Run on: March 24, 2003, 16:06:20 ; Search time 12 seconds

(without alignments)
902.110 Million cell updates/sec

Title: US-09-988-971-2

Perfect score: 261
Sequence: 1 MSLSPRRKSLPSPLSSSV.....RESLIFYSLNDEAVSLDA 261

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 112892 seqs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Query Length | ID | Description |
|------------|-------|-------|--------------|--------------|---------------------|
| 1 | 9 | 3.4 | 504 | 1 BLK_HUMAN | P51451 homo sapien |
| 2 | 9 | 3.4 | 552 | 1 SRC1_DROME | P00528 drosophila |
| 3 | 8 | 3.1 | 151 | 1 YN1S_WHEAT | P14723 triticum ae |
| 4 | 8 | 3.1 | 217 | 1 GRB2_HUMAN | Q13588 homo sapien |
| 5 | 8 | 3.1 | 217 | 1 GRB2_CHICK | Q07883 gallus galli |
| 6 | 8 | 3.1 | 217 | 1 GRB2_HUMAN | P29354 homo sapien |
| 7 | 8 | 3.1 | 217 | 1 GRB2_MOUSE | O60631 mus musculu |
| 8 | 8 | 3.1 | 217 | 1 GRB2_XENLA | P87379 xenopus lae |
| 9 | 8 | 3.1 | 461 | 1 PSSG_BOVIN | O46404 bos taurus |
| 10 | 8 | 3.1 | 461 | 1 PSSG_HUMAN | O92569 homo sapien |
| 11 | 8 | 3.1 | 461 | 1 PSSG_MOUSE | O64143 mus musculu |
| 12 | 8 | 3.1 | 503 | 1 HCK_RAT | P50545 rattus norv |
| 13 | 8 | 3.1 | 504 | 1 HCK_MACPA | Q95m30 macaca fasc |
| 14 | 8 | 3.1 | 507 | 1 LCK_CHICK | P42683 gallus galli |
| 15 | 8 | 3.1 | 511 | 1 LYN_HUMAN | P07948 homo sapien |
| 16 | 8 | 3.1 | 511 | 1 LYN_MOUSE | P25911 mus musculu |
| 17 | 8 | 3.1 | 511 | 1 LYN_RAT | O07014 rattus norv |
| 18 | 8 | 3.1 | 517 | 1 FGR_MOUSE | P14234 mus musculu |
| 19 | 8 | 3.1 | 524 | 1 HCK_MOUSE | P08103 mus musculu |
| 20 | 8 | 3.1 | 526 | 1 HCK_HUMAN | P08631 homo sapien |
| 21 | 8 | 3.1 | 529 | 1 FGR_HUMAN | P09769 homo sapien |
| 22 | 8 | 3.1 | 533 | 1 FYN_MOUSE | P39688 mus musculu |
| 23 | 8 | 3.1 | 1819 | 1 GCP6_HUMAN | O96rt7 homo sapien |
| 24 | 7 | 2.7 | 137 | 1 NS51_SOYBN | Q05544 glycine max |
| 25 | 7 | 2.7 | 137 | 1 RSVR_COTJA | P98162 coturnix co |
| 26 | 7 | 2.7 | 194 | 1 COAE_RHIME | O92te9 rhibobium m |
| 27 | 7 | 2.7 | 251 | 1 COX2_MARPO | P26857 marchantia |
| 28 | 7 | 2.7 | 269 | 1 TRIM_CANPA | P19236 canis famli |
| 29 | 7 | 2.7 | 293 | 1 IC66_HUMAN | P55212 homo sapien |
| 30 | 7 | 2.7 | 301 | 1 RNHL_MOUSE | O9cwy8 mus musculu |
| 31 | 7 | 2.7 | 345 | 1 OG61_HUMAN | O15527 homo sapien |
| 32 | 7 | 2.7 | 355 | 1 FXB8_HUMAN | Q14318 homo sapien |
| 33 | 7 | 2.7 | 355 | 1 FXB8_MOUSE | O35465 mus musculu |

| | | | | | |
|-----|---|-----|------|---------------|----------------------|
| 34 | 7 | 2.7 | 365 | 1 SOXB_RHOSO | P54997 rhodococcus |
| 35 | 7 | 2.7 | 394 | 1 HMPA_VIBRA | P40609 vibrio para |
| 36 | 7 | 2.7 | 473 | 1 ZF38_HUMAN | O9y586 homo sapien |
| 37 | 7 | 2.7 | 506 | 1 HETM_ANASP | P37693 anabesna sp |
| 38 | 7 | 2.7 | 544 | 1 YES_XIPHE | P27447 xiphophorus |
| 39 | 7 | 2.7 | 555 | 1 ZF38_MOUSE | Q07231 mus musculu |
| 40 | 7 | 2.7 | 594 | 1 NPAL_MOUSE | P97459 mus musculu |
| 41 | 7 | 2.7 | 597 | 1 ZF37_HUMAN | O9y6q3 homo sapien |
| 42 | 7 | 2.7 | 610 | 1 RCK2_YEAST | P38623 saccharomyc |
| 43 | 7 | 2.7 | 631 | 1 VG42_HAETN | P44236 haemophilus |
| 44 | 7 | 2.7 | 653 | 1 PABP_SCHRO | P31209 schizosach |
| 45 | 7 | 2.7 | 702 | 1 SPE1_ARATH | O96164 arabidopsis |
| 46 | 7 | 2.7 | 702 | 1 SPE2_ARATH | O82475 brassica ju |
| 47 | 7 | 2.7 | 711 | 1 SPE2_ARATH | O23141 arabidopsis |
| 48 | 7 | 2.7 | 743 | 1 Z267_HUMAN | O14586 homo sapien |
| 49 | 7 | 2.7 | 754 | 1 TBPE_YEAST | P40328 saccharomyc |
| 50 | 7 | 2.7 | 760 | 1 OCT1_XENLA | P16143 xenopus lae |
| 51 | 7 | 2.7 | 787 | 1 ITB6_MOUSE | O92019 mus musculu |
| 52 | 7 | 2.7 | 788 | 1 ITB6_HUMAN | P18564 homo sapien |
| 53 | 7 | 2.7 | 816 | 1 ATX1_HUMAN | P54253 homo sapien |
| 54 | 7 | 2.7 | 941 | 1 UVRA_SALTY | P37434 salmonella |
| 55 | 7 | 2.7 | 946 | 1 YBTE_YEAST | P38250 saccharomyc |
| 56 | 7 | 2.7 | 1117 | 1 YN96_YEAST | P53753 saccharomyc |
| 57 | 7 | 2.7 | 1426 | 1 CUR2_MOUSE | P70298 mus musculu |
| 58 | 7 | 2.7 | 1505 | 1 CUR2_HUMAN | O14529 homo sapien |
| 59 | 7 | 2.7 | 1666 | 1 MYM1_MOUSE | O62234 mus musculu |
| 60 | 7 | 2.7 | 1833 | 1 ZEP2_HUMAN | P31629 homo sapien |
| 61 | 7 | 2.7 | 2842 | 1 APC_RAT | P70478 rattus norv |
| 62 | 7 | 2.7 | 2843 | 1 APC_HUMAN | P25054 homo sapien |
| 63 | 7 | 2.7 | 2845 | 1 APC_MOUSE | O63315 mus musculu |
| 64 | 7 | 2.3 | 52 | 1 RL40_CHLRE | P14695 chlamydomon |
| 65 | 6 | 2.3 | 53 | 1 RL40_ORYSA | P35296 oryza sativ |
| 66 | 6 | 2.3 | 82 | 1 CS6A_BACSU | P54379 bacillus su |
| 67 | 6 | 2.3 | 86 | 1 Y425_TREPA | O83440 treponema p |
| 68 | 6 | 2.3 | 89 | 1 DBHB_NEIMA | O9jrt6 neisseria m |
| 69 | 6 | 2.3 | 90 | 1 TEGP_HSVB | P30025 simian herp |
| 70 | 6 | 2.3 | 91 | 1 DBHC_NEIMA | O9j310 neisseria m |
| 71 | 6 | 2.3 | 96 | 1 CH10_BUCMP | O51831 buchnera ap |
| 72 | 6 | 2.3 | 96 | 1 REV_SIVM | P36339 simian immu |
| 73 | 6 | 2.3 | 106 | 1 IATP_MOUSE | O35143 mus musculu |
| 74 | 6 | 2.3 | 108 | 1 IATP_RAT | O03344 rattus norv |
| 75 | 6 | 2.3 | 114 | 1 RLAI_HUMAN | O86954 thermotoga |
| 76 | 6 | 2.3 | 114 | 1 RLAI_RAT | P05386 homo sapien |
| 77 | 6 | 2.3 | 114 | 1 RLAI_RAT | P19944 rattus norv |
| 78 | 6 | 2.3 | 120 | 1 R18E_ARPE | O9y851 aetopyrum p |
| 79 | 6 | 2.3 | 122 | 1 YPDE_ECOLI | P76511 escherichia |
| 80 | 6 | 2.3 | 123 | 1 ELI2_PHYCR | P41803 phytophthor |
| 81 | 6 | 2.3 | 126 | 1 G8_HUMAN | O9ubae6 homo sapien |
| 82 | 6 | 2.3 | 128 | 1 U384_HSVMG | O05102 herpes' s dis |
| 83 | 6 | 2.3 | 130 | 1 YJ84_YEAST | P47151 saccharomyc |
| 84 | 6 | 2.3 | 133 | 1 ATPE_BACCHD | O9keh6 bacillus ha |
| 85 | 6 | 2.3 | 134 | 1 ATPE_RUMAL | O50143 ruminococcu |
| 86 | 6 | 2.3 | 135 | 1 YABO_METUA | O84880 methanococc |
| 87 | 6 | 2.3 | 137 | 1 MSCV_YERPE | O82383 yersinia pe |
| 88 | 6 | 2.3 | 137 | 1 TFX_METTH | O27001 methanobact |
| 89 | 6 | 2.3 | 137 | 1 TFX_METTH | P56811 methanobact |
| 90 | 6 | 2.3 | 141 | 1 NDK_AERPE | O9y8b0 aeropyrum p |
| 91 | 6 | 2.3 | 144 | 1 YOR5_KLEPE | O48451 klebsiella |
| 92 | 6 | 2.3 | 145 | 1 VG46_BPMU | O9tlv3 bacterioph |
| 93 | 6 | 2.3 | 147 | 1 YH83_SYNYA | P73602 synechocyst |
| 94 | 6 | 2.3 | 148 | 1 YCT9_YEAST | P25629 saccharomyc |
| 95 | 6 | 2.3 | 155 | 1 PA2X_HUMAN | O15496 homo sapien |
| 96 | 6 | 2.3 | 158 | 1 FXSA_ECOLI | P37147 escherichia |
| 97 | 6 | 2.3 | 163 | 1 LCA_RAT | P00714 rattus norv |
| 98 | 6 | 2.3 | 163 | 1 YOR3_EAV | P28893 equine arte |
| 99 | 6 | 2.3 | 165 | 1 CGHB_HUMAN | P01233 homo sapien |
| 100 | 6 | 2.3 | 166 | 1 RELD_PANTR | P51455 pan troglod |

ALIGNMENTS

RESULT 1

BLK_HUMAN
ID BLK_HUMAN STANDARD: PRT; 504 AA.
AC P51451; Q16291;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase BLK (EC 2.7.1.112) (B lymphocyte kinase) (p55-BLK).
GN BLK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95148218; PubMed=7822795;
RA Islam K.B., Rabbani H., Larson C., Sanders R., Smith C.I.;
RT "Molecular cloning and chromosomal localization of the human homologue of a B-lymphocyte specific protein tyrosine kinase (blk).";
RL Oncogene 10:477-486(1995).
CC -1- FUNCTION: BLK MAY FUNCTION IN A SIGNAL TRANSDUCTION PATHWAY THAT IS RESTRICTED TO B LYMPHOID CELLS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.

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CC EMBL: Z33998; CAA83965.1; -;
DR EMBL: S76617; AAB33265.1; -;
DR HSSP: P16277; BLK.
DR Genew; HGNC:1057; BLK.
DR MIM; 191305; -;
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR000980; SH2.
DR InterPro; IPR001452; SH3.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; kinase; 1.
DR PRINTS; PRO0401; SH2DOMAIN.
DR PRINTS; PRO0452; SH3DOMAIN.
DR PRINTS; PRO0109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TYRK; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN KINASE TYR; FALSE_NEG.
DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW Tyrosine-protein kinase; Phosphorylation; Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain.

FT INIT MET 0 0 BY SIMILARITY.
FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
FT DOMAIN 57 117 SH3.
FT DOMAIN 123 219 SH2.
FT DOMAIN 240 493 PROTEIN KINASE.
FT NP_BIND 246 254 ATP (BY SIMILARITY).
FT BINDING 268 268 ATP (BY SIMILARITY).
FT ACT_SITE 359 359 BY SIMILARITY.
FT MOD_RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT CONFLICT 286 286 M -> V (IN REF. 2).
FT CONFLICT 406 406 I -> Y (IN REF. 2).
SQ SEQUENCE 504 AA; 57607 MW; 5BBD1F50EC7370C8 CRC64;

Query Match 3.4%; Score 9; DB 1; Length 504;
Best Local Similarity 100.0%; Pred. No. 0.78;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 165 TFPISLQALV 173
DB 193 TFPISLQALV 201

RESULT 2
SRC1_DROME STANDARD: PRT; 552 AA.
AC P00528; Q18372; Q9VZ42;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase Src64B (EC 2.7.1.112).
DE SRC64B OR SRC1 OR CG7524.
GN Drosophila melanogaster (Fruit fly).
OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Braachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
[1]
RP SEQUENCE FROM N.A.. FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STRGE.
RX MEDLINE=86028179; PubMed=2996778;
RA Simon M.A., Drees B., Kornberg T., Bishop J.M.;
RT "The nucleotide sequence and the tissue-specific expression of Drosophila C-src".
RL Cell 42:831-840(1985).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkeley;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G., An J.F., Agbayani A., An H.-U., Andrews-Fiankoch C., Balwin D., Ballaw R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.W., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolintsov S., Borokova D., Botchan M.R., Bouck J., Brockstein P., Brottier P., Burris K.C., Buser D.A., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., Dea P., Delcher A., Deng Z., Drenth J., Dew I., Diez S.M., Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W., Finkler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Goad C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Isegam C., Jajmal M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kjelbel B.E., Kohler C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Laso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Martel B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Mishaeva N.V., Mobarry C., Morris U., Mostrelet A., Mount S.M., Moy W., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Vairaks R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weisenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of *Drosophila melanogaster*,"
 Science 287:2185-2195 (2000).
 RL [3]
 RN SEQUENCE OF 249-552 FROM N.A.
 RX MEDLINE=84082064; PubMed=6317185.
 RA Hoffmann F.M., Fresco L.D., Hoffman-Palk H., Shilo B.-Z.,
 RT "Nucleotide sequences of the *Drosophila* src and abl homologs:
 RT conservation and variability in the src family oncogenes,"
 Cell 35:393-401 (1983).
 RL [4]
 RN SEQUENCE OF 410-461 FROM N.A.
 RX MEDLINE=98401146; PubMed=9731193.
 RA Gates A.C., Wollberg P., Achen W.G., Wilks A.F.,
 RT "Sampling the genomic pool of protein tyrosine kinase genes using the
 RT polymerase chain reaction with genomic DNA,"
 Biochem. Biophys. Res. Commun. 249:660-667 (1998).
 RL [5]
 RN FUNCTION: May play a role in the development of neural tissue and
 RN smooth muscle.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC -1- tyrosine phosphate.
 CC -1- TISSUE SPECIFICITY: After the first 8 hr of development,
 CC accumulates almost exclusively in neural tissues such as the
 CC brain, ventral nerve chord, and eye-antennal discs, and in
 CC differentiating smooth muscle.
 CC -1- DEVELOPMENTAL STAGE: Abundant in embryos and pupae, rare in larvae
 CC and adults.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUPRANILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 DR EMBL: M11917; AAA28913.1; -
 DR EMBL: AE003481; AA47922.1; -
 DR EMBL: K01043; AA28489.1; -
 DR EMBL: AJ002919; CA05754.1; -
 DR PIR: A00634; TRPS.
 DR HSP: P11362; TRPS.
 DR FLYbase: Fgn0003501; Src64B.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR002290; Ser_thr_pkinase.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00326; SH3; 1.

DR SMART: SM00220; S TKC; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE: PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE: PS50011; PROTEIN KINASE_DOM; 1.
 DR PROSITE: PS50011; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Kinase; Tyrosine-protein kinase; Proto-oncogene; Phosphorylation;
 KW Transferase; ATP-binding; SH3 domain; SH2 domain;
 KW Developmental protein
 KW Domain 95 156
 FT DOMAIN 162 259
 FT SH2.
 FT DOMAIN 284 537
 FT SH3.
 FT NP BIND 290 298
 FT ATP (BY SIMILARITY).
 FT BINDING 312 312
 FT ACT SITE 404 404
 FT MOD RES 434 434
 FT CONFLICT 102 102
 FT CONFLICT 261 263
 FT CONFLICT 266 269
 FT CONFLICT 272 272
 FT CONFLICT 272 272
 FT CONFLICT 286 287
 FT CONFLICT 290 290
 FT CONFLICT 293 293
 FT CONFLICT 316 316
 FT CONFLICT 316 316
 FT CONFLICT 365 366
 FT CONFLICT 373 373
 FT CONFLICT 384 385
 FT CONFLICT 389 390
 FT CONFLICT 393 393
 FT CONFLICT 400 400
 FT CONFLICT 406 407
 FT CONFLICT 435 435
 FT CONFLICT 460 460
 FT CONFLICT 471 471
 FT CONFLICT 484 484
 FT CONFLICT 507 507
 FT CONFLICT 536 536
 FT CONFLICT 536 536
 FT SEQUENCE 552 AA; 63002 MW; 4A63CF4F1562864 CRC64;
 Query Match 3.4%; Score 9; DB 1; Length 552;
 Best Local Similarity 100.0%; Pred. No. 0.85;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 165 TRPSLOALV 173
 DB 233 TRPSLOALV 241
 RESULT 3
 TWIS WHEAT STANDARD; PRT; 151 AA.
 AC P14723;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical 16 kDa protein in middle repetitive insertion sequence
 DE WIS1.
 OS Triticum aestivum (Wheat).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OC NCBI_TaxID=4585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Chinese Spring;
 RX MEDLINE=89364725; PubMed=2549380;
 RA Martensen R.A., Baulcombe D.C.;
 RT "An unusual wheat insertion sequence (WIS1) lies upstream of an
 RT alpha-amylase gene in hexaploid wheat, and carries a 'minisatellite'
 RT array,"
 RL Mol. Gen. Genet. 217:401-410 (1989).
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DR EMBL: X15870; CAJ33890.1; -.
 DR PIR: S10084; S10084.
 KW Transposable element, Hypothetical protein.
 SQ SEQUENCE 151 AA; 15950 MW; 3BA330BD31EC6742 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 151;
 Best Local Similarity 100.0%; Pred. No. 2.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LPSPLSS 18
 Db 22 LPSPLSS 29

RESULT 4
 ID GRAP HUMAN STANDARD; PRT; 217 AA.
 AC Q13588.
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DE 15-JUN-2002 (Rel. 41, Last annotation update)
 GN GRB2-related adaptor protein.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96218119; PubMed=8647802;
 RX Feng G.-S., Ouyang Y.-B., Hu D.-P., Shi Z.-Q., Gentz R., Ni J.;
 RT "Grp is a novel SH3-SH2-SH3 adaptor protein that couples tyrosine
 RT kinases to the Ras pathway."
 RL J. Biol. Chem. 271:12129-12132(1996)

CC -1- FUNCTION: COUPLE SIGNALS FROM RECEPTOR AND CYTOPLASMIC TYROSINE
 CC KINASES TO THE RAS SIGNALING PATHWAY.
 CC -1- SUBUNIT: ASSOCIATES THROUGH ITS SH2 DOMAIN WITH LIGAND-ACTIVATED
 CC RECEPTORS FOR STEM CELL FACTOR (KIT) AND ERYTHROPOIETIN (EPO).
 CC ALSO FORMS A STABLE COMPLEX WITH THE BCR-ABL ONCOPROTEIN. GRAP IS
 CC ASSOCIATED WITH THE RAS GUANINE NUCLEOTIDE EXCHANGE FACTOR SOS1,
 CC PRIMARILY THROUGH ITS N-TERMINAL SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.

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DR EMBL: U52518; AAC50541.1; -.
 DR HSSP: O60631; IGB0.
 DR Genew: HGNC:4562; GRAP.
 DR MIM: 604330; -.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR ProDom: PD000066; SH3; 2.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.

DR SMART: SM00326; SH3; 2.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 2.
 KW SH2 domain; SH3 domain; Repeat.
 FT DOMAIN 1 58 SH3 1.
 FT DOMAIN 60 152 SH2.
 FT DOMAIN 156 215 SH3 2.
 SQ SEQUENCE 217 AA; 25336 MW; 09FEC2FBAC0FAF8 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 217;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFLIRS 123
 Db 81 GAFLIRS 88

RESULT 5
 ID GRB2_CHICK STANDARD; PRT; 217 AA.
 AC Q07883;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth factor receptor-bound protein 2 (GRB2 adapter protein)
 GN GRB2
 OS Gallus gallus (chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archaeopteryx; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=94085795; PubMed=8262390;
 RX Maennle V.-M., Merilainen J., Lento V.-P.;
 RL "Sequence of a chicken cDNA encoding a GRB2 protein."
 RL Gene 134:299-300(1993).

CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH
 CC AS IRS-1, SHC AND LNK. PROBABLY VIA THE CONCERTED ACTION OF BOTH
 CC ITS SH2 AND SH3 DOMAINS, IT ALSO SEEMS TO INTERACT WITH RAS
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.
 CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE AND CELL DISTRIBUTION.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.

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DR EMBL: L19258; AAA16318.1; -.
 DR PIR: J10664; J10664.
 DR HSSP: P29354; IGR1.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR PRINTS: PR00452; SH3DOMAIN.

DR P10dom, P0000066; SH3; 2.
 DR P10dom, P0000093; SH2; 1.
 DR SMART; SM00326; SH2; 1.
 DR SMART; SM00326; SH3; 2.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 2.
 KW SH2 domain; SH3 domain; Repeat.
 FT DOMAIN 1 58 SH3 1.
 FT DOMAIN 60 152 SH2 1.
 FT DOMAIN 156 215 SH3 2.
 SQ SEQUENCE 217 AA; 25076 MW; DDC9A84ECDC52859 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 217;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 116 GAFIRES 123
 Db 81 GAFIRES 88

RESULT 6
 GRB2 HUMAN STANDARD; PRT; 217 AA.
 ID GRB2 HUMAN STANDARD; PRT; 217 AA.
 AC P29354; Q63057; Q14450;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Growth factor receptor-bound protein 2 (GRB2 adapter protein)
 DE (SH2/SH3 adapter GRB2) (ASH protein).
 GN GRB2 OR ASH.
 OS Homo sapiens (Human); and
 OS Rattus norvegicus (Rat); and
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606; 10116;
 RX NCBI_TaxID=9606; 10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Brain;
 RX MEDLINE=92354060; PubMed=1322798;
 RA Lowenstein E.J., Daly R.J., Batzer A.G., Li W., Margolis B.,
 RA Lammers R., Ullrich A., Skolnik E.Y., Bar-Sagi D., Schlessinger J.;
 RT "The SH2 and SH3 domain-containing protein GRB2 links receptor
 RT tyrosine kinases to ras signaling.";
 RL Cell 70:431-442(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human, and Rat; TISSUE=Brain, and Lung;
 RX MEDLINE=93028395; PubMed=1384039;
 RA Matsumoto K., Yamakawa A., Shibata M., Takenawa T.;
 RT "Cloning of ASH, a ubiquitous protein composed of one Src homology
 RT region (SH) 2 and two SH3 domains, from human and rat cDNA
 RT libraries.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:9015-9019(1992).
 RN [3]
 RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
 RC SPECIES=Rat; STRAIN=Mistar; TISSUE=Brain;
 RX MEDLINE=95293967; PubMed=775428;
 RA Watanabe K., Fukuchi T., Hosoya H., Shirasawa T., Matsuda K.,
 RA Miki H., Takenawa T.;
 RT "Splicing isoforms of rat Ash/Grb2. Isolation and characterization of
 RT the cDNA and genomic DNA clones and implications for the
 RT physiological roles of the isoforms.";
 RL J. Biol. Chem. 270:13733-13739(1995).
 RN [4]
 RP SEQUENCE FROM N.A. (ISOPFORM GRB3-3).
 RC SPECIES=Human; TISSUE=Placenta;
 RX MEDLINE=94233382; PubMed=8178156;
 RA Fath T., Schweighofer F., Rey I., Mulon M.C., Boiziau J.,
 RA Duchesne M., Tocque B.;
 RT "Cloning of a Grb2 isoform with apoptotic properties.";
 RL Science 264:971-974(1994).
 RN [5]

RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Epidermis;
 RX MEDLINE=99162407; PubMed=10051406;
 RA Boeckmann H., Gehring S., Jaros W.;
 RT "The gene structure of the human growth factor bound protein GRB2.";
 RL Genomics 56:203-207(1999).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Human; TISSUE=Lymph;
 RA Struhsberg R.;
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP ASSOCIATION WITH IRS-1.
 RX MEDLINE=9326568; PubMed=8388384;
 RA Tobe K., Matsumoto K., Tamemoto H., Ueki K., Kaburagi Y., Asai S.,
 RA Noguchi T., Tanaka M., Tanaka S., Hattori S., Fukui Y., Akanuma Y.,
 RA Yazaki Y., Takenawa T., Kodawaki T.;
 RT "Insulin stimulates association of insulin receptor substrate-1 with
 RT the protein abundant Src homology/growth factor receptor-bound
 RT protein 2.";
 RL J. Biol. Chem. 268:11167-11171(1993).
 RN [8]
 RP ASSOCIATION WITH IRS-1 AND SHC.
 RX MEDLINE=93259135; PubMed=8491186;
 RA Skolnik E.Y., Lee C.-H., Batzer A., Vicentini L.M., Zhou M., Daly R.,
 RA Myers M.J., Jr., Backer J.M., Ullrich A., White M.F., Schlessinger J.;
 RT "The SH2/SH3 domain-containing protein GRB2 interacts with tyrosine-
 RT phosphorylated IRS1 and Shc: implications for insulin control of ras
 RT signaling.";
 RL EMBO J. 12:1929-1936(1993).
 RN [9]
 RP STRUCTURE BY NMR OF 1-56.
 RX MEDLINE=97280795; PubMed=935122;
 RA Wittekind M., Mapelli C., Lee V., Goldfarb V., Friedrichs M.S.,
 RA Meyers C.A., Mueller L.;
 RT "Solution structure of the Grb2 N-terminal SH3 domain complexed with
 RT a ten-residue peptide derived from SOS: direct refinement against
 RT NOESY-J-couplings and 1H and 13C chemical shifts.";
 RL J. Mol. Biol. 267:933-952(1997).
 RN [10]
 RP STRUCTURE BY NMR OF 60-158.
 RX MEDLINE=96387228; PubMed=8794768;
 RA Thornton K.H., Mueller W.T., McConnell P., Zhu G., Saliel A.R.,
 RA Tharabai V.;
 RT "Nuclear magnetic resonance solution structure of the growth factor
 RT receptor-bound protein 2 Src homology 2 domain.";
 RL Biochemistry 35:11852-11864(1996).
 RN [11]
 RP STRUCTURE BY NMR OF 53-163.
 RA Senior M.M., Frederick A.F., Black S., Murgolo N.J., Perkins L.M.,
 RA Wilson O., Shaw M.E., Wang Y.-S.;
 RT "The three-dimensional solution structure of the Src homology domain-2
 RT of the growth factor receptor-bound protein-2.";
 RL J. Biomol. NMR 11:153-164(1998).
 RN [12]
 RP STRUCTURE BY NMR OF 159-215.
 RX MEDLINE=95187706; PubMed=7881903;
 RA Kohda D., Terasawa H., Ichikawa S., Ogura K., Hatanaka H.,
 RA Mandiyan V., Ullrich A., Schlessinger J., Inagaki F.;
 RT "Solution structure and ligand-binding site of the carboxy-terminal
 RT SH3 domain of GRB2.";
 RL Structure 2:1029-1040(1994).
 RN [13]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS).
 RX MEDLINE=95232505; PubMed=7716522;
 RA Maignan S., Guilloteau J.P., Fromage N., Arnoux B., Becquart J.,
 RA Duchoux A.;
 RT "Crystal structure of the mammalian Grb2 adaptor.";
 RL Science 268:291-295(1995).
 RN [14]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS) OF 56-153.
 RX MEDLINE=98308003; PubMed=9642078;
 RA Rahuel J., Garcia-Echeverria C., Furet P., Straus A., Caravatti G.,

RA Fretz H., Schoepfer J., Gay B.,
 RT "Structural basis for the high affinity of amino-aromatic SH2
 RT phosphopeptide ligands.";
 RL J. Mol. Biol. 279:1013-1022 (1998).
 RN [15]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 49-163.
 RX MEDLINE=9912587; PubMed=1009780;
 RA Etmeayer P., France D., Gonarides J., Jarosinski M., Martin M.-S.,
 RA Rondeau J.-M., Sabio S., Topiol S., Weidmann B., Zurini M., Balz K.W.;
 RT "Structural and conformational requirements for high-affinity binding
 RT to the SH2 domain of Grb2(1)." ;
 RL J. Med. Chem. 42:971-980 (1999).
 RN [16]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 57-152.
 RX MEDLINE=99324016; PubMed=10395476;
 RA Furet P., Garcia-Scheverria C., Gay B., Schoepfer J., Zeller M.,
 RA Rahuel J.;
 RT "Structure-based design, synthesis, and X-ray crystallography of a
 RT high-affinity antagonist of the Grb2-SH2 domain containing an
 RT asparagine mimetic." ;
 RL J. Med. Chem. 42:2358-2363 (1999).
 CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH
 CC AS IRS-1, SHC AND LNK; PROBABLY VIA THE CONCERTED ACTION OF BOTH
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.
 CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.
 CC -1- FUNCTION: ISOFORM GRB3-3 DOES NOT BIND TO PHOSPHORYLATED EPIDERMAL
 CC GROWTH FACTOR RECEPTOR (EGFR) BUT INHIBITS EGF-INDUCED
 CC TRANSACTIVATION OF A RAS-RESPONSIVE ELEMENT. GRB3-3 ACTS AS A
 CC DOMINANT NEGATIVE PROTEIN OVER GRB2 AND BY SUPPRESSING
 CC PROLIFERATIVE SIGNALS, MAY TRIGGER ACTIVE PROGRAMMED CELL DEATH.
 CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: WIDE TISSUE AND CELL DISTRIBUTION.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
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 CC -----
 DR EMBL; M66995; AAA58448.1; -;
 DR EMBL; X62853; CAAA4664.1; -;
 DR EMBL; X62853; CAAA4665.1; -;
 DR EMBL; D49846; BAA08645.1; -;
 DR EMBL; D49846; BAA08645.1; -;
 DR EMBL; L29511; AAC37549.1; -;
 DR EMBL; AF063618; AAC72075.1; -;
 DR EMBL; AF063614; AAC72075.1; JOINED.
 DR EMBL; AF063615; AAC72075.1; JOINED.
 DR EMBL; AF063616; AAC72075.1; JOINED.
 DR EMBL; AF063617; AAC72075.1; JOINED.
 DR EMBL; BC006311; AAH00631.1; -;
 DR PIR; A43321; A43321.
 DR PIR; S26050; S26050.
 DR PDB; 1GRI; 08-MAR-96.
 DR PDB; 1GFC; 31-AUG-94.
 DR PDB; 1GFD; 31-AUG-94.
 DR PDB; 1GHU; 27-JAN-97.
 DR PDB; 1TZE; 07-JUL-97.
 DR PDB; 1FHS; 17-JUN-98.
 DR PDB; 1BM2; 05-AUG-98.

DR PDB; 1BM2; 29-JUL-98.
 DR PDB; 1ZFP; 30-MAR-99.
 DR PDB; 1CJ1; 22-DEC-99.
 DR Genew; HGNC:4566; GRB2.
 Query Match 3.1%; Score 8; DB 1; Length 217;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 116 GARLINES 123
 Db 81 GARLINES B8
 RESULT 7
 GRB2 MOUSE STANDARD; PRT; 217 AA.
 AC 060631; 061240;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Growth factor receptor-bound protein 2 (GRB2 adapter protein)
 DE (SH2/SH3 adapter GRB2).
 GN GRB2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BAB/c;
 RX MEDLINE=93360985; PubMed=7689150;
 RA Shen K., Bustelo X.R., Rawson T., Barbacid M.;
 RT "Molecular cloning of the mouse grb2 gene: differential interaction
 RT of the grb2 adapter protein with epidermal growth factor and nerve
 RT growth factor receptors." ;
 RL Mol. Cell. Biol. 13:5500-5512 (1993).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM GRB3-3).
 RC STRAIN=BAB/c;
 RA Tanaka S.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP STRUCTURE BY NMR OF 1-59.
 RX MEDLINE=97280795; PubMed=9335122;
 RA Wittekind M., Mepelli C., Lee V., Goldfarb V., Friedrichs M.S.,
 RA Meyers C.A., Mueller L.;
 RT "Solution structure of the Grb2 N-terminal SH3 domain complexed with
 RT a ten-residue peptide derived from SOS: direct refinement against
 RT NOES, J-couplings and 1H and 13C chemical shifts." ;
 RL J. Mol. Biol. 267:933-952 (1997).
 CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF
 CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO
 CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH
 CC AS IRS-1, SHC AND LNK; PROBABLY VIA THE CONCERTED ACTION OF BOTH
 CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS
 CC IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS. BINDS TO AND
 CC TRANSLOCATES THE GUANINE NUCLEOTIDE EXCHANGE FACTORS SOS.
 CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM
 CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR
 CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS
 CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A
 CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE.
 CC -1- FUNCTION: ISOFORM GRB3-3 DOES NOT BIND TO PHOSPHORYLATED EPIDERMAL
 CC GROWTH FACTOR RECEPTOR (EGFR) BUT INHIBITS EGF-INDUCED
 CC TRANSACTIVATION OF A RAS-RESPONSIVE ELEMENT. GRB3-3 ACTS AS A
 CC DOMINANT NEGATIVE PROTEIN OVER GRB2 AND BY SUPPRESSING
 CC PROLIFERATIVE SIGNALS, MAY TRIGGER ACTIVE PROGRAMMED CELL DEATH
 CC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS ARE PRODUCED BY
 CC ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.

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CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U07617; AAB40022.1; -
CC EMBL: D85748; BAA12862.1; -
CC PDB: 1GBQ; 04-SEP-97.
CC PDB: 2GBQ; 04-SEP-97.
CC PDB: 3GBQ; 04-SEP-97.
CC PDB: 4GBQ; 04-SEP-97.
CC PDB: 1GBR; 26-JAN-95.
CC MGD: MGI:95805; Gtd2.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001452; SH3.
CC Pfam: PF00017; SH2; 1.
CC Pfam: PF00018; SH3; 2.
CC PRINTS: PR00401; SH2DOMAIN.
CC PRINTS: PR00452; SH3DOMAIN.
CC ProDom: PD000066; SH3; 2.
CC ProDom: PD000093; SH2; 1.
CC SMART: SM00252; SH2; 1.
CC SMART: SM00326; SH3; 2.
CC PROSITE: PS50001; SH2; 1.
CC PROSITE: PS50002; SH3; 2.
CC SH2 domain; SH3 domain; Repeat; Alternative splicing; 3D-structure.
FT DOMAIN 1 58 SH3 1.
FT DOMAIN 60 152 SH2 2.
FT DOMAIN 156 215 SH3 2.
FT VASAPLIC 60 100 MISSING (IN ISOFORM GRB3-3).
SQ SEQUENCE 217 AA; 25238 MW; 97F4A4FE4B248DDF CRC64;

Query Match 3.1%; Score 8; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRES 123
DB 81 GAFLIRES 88

RESULT 8
GRB2_XENLA STANDARD; PRT; 217 AA.
ID GRB2_XENLA
AC P87379;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Growth factor receptor-bound protein 2 (GRB2 adapter protein)
DE (SH2/SH3 adapter GRB2).
GN GRB2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodidae; Xenopus.
OC NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Lu W., Mayer B.J.;
RL Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: ASSOCIATES WITH ACTIVATED TYROSINE-PHOSPHORYLATED EGF
CC RECEPTORS AND PDGF RECEPTORS VIA ITS SH2 DOMAIN. GRB2 ALSO
CC ASSOCIATES TO OTHER CELLULAR TYROSINE-PHOSPHORYLATED PROTEINS SUCH
CC AS IRS-1, SHC AND LNK. PROBABLY VIA THE COORDINATED ACTION OF BOTH
CC ITS SH2 AND SH3 DOMAINS. IT ALSO SEEMS TO INTERACT WITH RAS
CC PROTEIN IN THE SIGNALING PATHWAY LEADING TO DNA SYNTHESIS (BY
CC SIMILARITY).
CC -1- FUNCTION: PROBABLY REPRESENTS A REGULATORY SUBUNIT OF DOWNSTREAM

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CC SIGNALING MOLECULES WHOSE ACTIVITY IS MODULATED BY RECEPTOR
CC BINDING. A 55 KDA PHOSPHOPROTEIN OF UNKNOWN FUNCTION WHICH BINDS
CC TO GRB2 IN RESPONSE TO GROWTH FACTOR STIMULATION COULD BE A
CC DOWNSTREAM SIGNALING MOLECULE CANDIDATE (BY SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 2 SH3 DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE GRB2 / SEM-5 / DRK FAMILY.
CC
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CC
CC EMBL: U89775; AAB49699.1; -
CC HSSP: P29354; IGHU.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001452; SH3.
CC Pfam: PF00017; SH2; 1.
CC Pfam: PF00018; SH3; 2.
CC PRINTS: PR00452; SH3DOMAIN.
CC ProDom: PD000066; SH3; 2.
CC ProDom: PD000093; SH2; 1.
CC SMART: SM00252; SH2; 1.
CC SMART: SM00326; SH3; 2.
CC PROSITE: PS50001; SH2; 1.
CC PROSITE: PS50002; SH3; 2.
CC SH2 domain; SH3 domain; Repeat.
FT DOMAIN 1 58 SH3 1.
FT DOMAIN 60 152 SH2 2.
FT DOMAIN 156 215 SH3 2.
SQ SEQUENCE 217 AA; 25104 MW; 1622802ED26CE46A CRC64;

Query Match 3.1%; Score 8; DB 1; Length 217;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLIRES 123
DB 81 GAFLIRES 88

RESULT 9
P55G_BOVIN STANDARD; PRT; 461 AA.
ID P55G_BOVIN
AC O46404;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-kinase
DE p85-gamma subunit) (PtdIns-3-kinase p85-gamma) (p55PIK).
GN PI3K.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OC NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adrenal cortex;
RA Varnal P., Balla T.;
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
CC KINASES THROUGH ITS SH2 DOMAIN AND REGULATES THEIR KINASE
CC ACTIVITY. DURING INSULIN STIMULATION, IT ALSO BINDS TO IRS-1.
CC SUBUNIT. HETERODIMER OF A P110 (CATALYTIC) AND A P55 (REGULATORY)
CC SUBUNITS.
CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND TESTIS. LOWER
CC LEVELS IN ADIPOSE TISSUE, KIDNEY, HEART, LUNG AND SKELETAL MUSCLE.
CC BARELY DETECTABLE IN LIVER AND SPLEEN.

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CC -1- SIMILARITY: BELONGS TO THE PI3K P85 SUBUNIT FAMILY.
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -----
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 CC -----
 CC EMBL: AF036256; AAB8704.1; -
 DR HSSP: P23727; 2PMB.
 DR InterPro: IPR001720; PI3K_kinase_p85.
 DR InterPro: IPR000980; SH2.
 DR Pfam: PF00017; SH2; 2.
 DR PRINTS: PR00678; PI3KINASEP85.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000093; SH2; 2.
 DR SMART: SM00252; SH2; 2.
 DR SMART: PS50001; SH2; 2.
 DR SH2 domain; Repeat; Phosphorylation.
 FT DOMAIN 65 160 SH2 1.
 FT MOD RES 358 452 SH2 2.
 FT MOD RES 341 341 PHOSPHORYLATION (BY SIMILARITY).
 SQ SEQUENCE 461 AA; 54388 MW; C5B77282B9A96DAD CRC64;
 Query Match 3.1%; Score 8; DB 1; Length 461;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 116 GAFLIRES 123
 Db 378 GAFLIRES 385
 RESULT 10
 P55G_HUMAN STANDARD; PRT; 461 AA.
 ID P55G_HUMAN STANDARD; PRT; 461 AA.
 AC Q92569; O60482;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-kinase
 DE p85-gamma subunit) (Pcdins-3-kinase p85-gamma) (p55PIK).
 GN PIK3R3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Suzuki T.;
 RT "Molecular cloning of human p55piK".
 RT Submitted (OCT-1996) to the EMBL/Genbank/DBJ databases.
 RU [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
 RC TISSUE=Petal brain;
 RX MEDLINE=98192526; PubMed=9524259;
 RX Dey B.R., Furlanetto R.W., Nisley S.P.;
 RT "Cloning of human p55 gamma, a regulatory subunit of
 RT phosphatidylinositol 3-kinase, by a yeast two-hybrid library screen
 RT with the insulin-like growth factor-I receptor".
 RU Gene 209:175-183(1998).
 CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
 CC KINASES THROUGH ITS SH2 DOMAIN AND REGULATES THEIR KINASE
 CC ACTIVITY. DURING INSULIN STIMULATION, IT ALSO BINDS TO IRS-1.
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNIT.
 CC -1- ALTERNATIVE PRODUCTS: 3 ISOFORMS: 1 (SHOWN HERE), 2 AND 3; ARE
 CC PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND TESTIS. LOWER
 CC LEVELS IN ADIPOSE TISSUE, KIDNEY, HEART, LUNG AND SKELETAL MUSCLE.

CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: HIGH, WITH OTHER P85 SUBUNITS, AND WITH P85-ALPHA AND
 CC P85-BETA SUBUNITS.
 CC -----
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 CC -----
 CC EMBL: D88532; BAAL3636.1; -
 DR EMBL: AF028785; AAC39696.1; -
 DR HSSP: P23727; 2PMB.
 DR Genew: HGNC:8981; PIK3R3.
 DR MIM: 606076; -
 DR InterPro: IPR001720; PI3K_kinase_p85.
 DR InterPro: IPR000980; SH2.
 DR Pfam: PF00017; SH2; 2.
 DR PRINTS: PR00678; PI3KINASEP85.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR ProDom: PD000093; SH2; 2.
 DR SMART: SM00252; SH2; 2.
 DR SMART: PS50001; SH2; 2.
 DR SH2 domain; Repeat; Phosphorylation; Alternative splicing.
 FT DOMAIN 34 44 PRO-RICH.
 FT DOMAIN 65 160 SH2 1.
 FT MOD RES 358 452 SH2 2.
 FT VARSEPLC 36 71 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSEPLC 256 314 MISSING (IN ISOFORM 3).
 FT CONFLICT 21 21 P -> L (IN REF. 2).
 SQ SEQUENCE 461 AA; 54462 MW; C03CEFF22EB50B9 CRC64;
 Query Match 3.1%; Score 8; DB 1; Length 461;
 Best Local Similarity 100.0%; Pred. No. 6.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 116 GAFLIRES 123
 Db 378 GAFLIRES 385
 RESULT 11
 P55G_MOUSE STANDARD; PRT; 461 AA.
 ID P55G_MOUSE STANDARD; PRT; 461 AA.
 AC Q64143;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Phosphatidylinositol 3-kinase regulatory gamma subunit (PI3-kinase
 DE p85-gamma subunit) (Pcdins-3-kinase p85-gamma) (p55PIK).
 GN PIK3R3.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Scurionathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=95349612; PubMed=7542745;
 RX Pons S., Asano T., Glasheen E., Mizalpeix M., Zhang Y., Fisher T.L.,
 RA Wiers M.G. Jr., Sun X.J., White M.P.;
 RT "The structure and function of p55piK reveal a new regulatory subunit
 RT for phosphatidylinositol 3-kinase".
 RU Mol. Cell. Biol. 15:4453-4465(1995).
 CC -1- FUNCTION: BINDS TO ACTIVATED (PHOSPHORYLATED) PROTEIN-TYROSINE
 CC KINASES THROUGH ITS SH2 DOMAIN AND REGULATES THEIR KINASE
 CC ACTIVITY. DURING INSULIN STIMULATION, IT ALSO BINDS TO IRS-1.
 CC -1- SUBUNIT: HETERODIMER OF A P110 (CATALYTIC) AND A P85 (REGULATORY)
 CC SUBUNIT.
 CC -1- TISSUE SPECIFICITY: HIGHEST LEVELS IN BRAIN AND TESTIS. LOWER


```
CC LEVELS IN ADIPOSE TISSUE, KIDNEY, HEART, LUNG AND SKELETAL MUSCLE.
CC BARELY DETECTABLE IN LIVER AND SPLEEN.
CC -1- SIMILARITY: BELONGS TO THE PI3K P85 SUBUNIT FAMILY.
CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
CC -----
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CC -----
CC EMBL; S79169; AAB34938.1; -.
CC HSSP; P23727; 2PMB.
CC DR MGD; MGI:109277; P1K3r3.
CC DR InterPro; IPR001720; PI3kinase_P85.
CC DR InterPro; IPR000980; SH2.
CC DR Pfam; PF00017; SH2; 2.
CC DR PRINTS; PR00676; PI3KINASEP85.
CC DR PRINTS; PR00401; SH2DOMAIN.
CC DR ProDom; PD000093; SH2; 2.
CC DR SMART; SM00252; SH2; 2.
CC DR PROSITE; PS50001; SH2; 2.
CC KW SH2 domain; Repeat; Phosphorylation.
CC FT DOMAIN 65 160 SH2 1.
CC FT DOMAIN 358 452 SH2 2.
CC FT MOD RES 341 341 PHOSPHORYLATION.
CC SQ SEQUENCE 461 AA; 54474 MW; 97A01ADDFAPAC661F CRC64;

Query Match 3.1%; Score 8; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFLRES 123
Db 378 GAFLRES 385

RESULT 12
HCK_RAT
ID ID_HCK_RAT STANDARD; PRT; 503 AA.
AC P50545; O64647;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
DE kinase).
DE GN HCK.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92109719; PubMed=1764064;
RA Okano Y., Sugimoto Y., Fukuoaka M., Matsui A., Nagata K.I., Nozawa Y.;
RT "Identification of rat cDNA encoding hck tyrosine kinase from
RT megakaryocytes.";
RT Biochem. Biophys. Res. Commun. 181:1137-1144 (1991).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar; TISSUE=Spleen;
RA Vijaya Gouri B.S., Rema V., Kamalakar S., Swarup G.;
RT "Nucleotide sequence of a cDNA coding for rat hck tyrosine kinase and
RT characterization of its gene product.";
RT J. Biosci. 19:117-129 (1994).
CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
CC DEGRADATION PROCESS OF NEUTROPHILS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
```

```
CC -1- SUBCELLULAR LOCATION: Membrane-associated.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
CC EMBL; S74141; AAB20754.1; -.
CC DR EMBL; M83666; AAA4312.1; -.
CC DR EMBL; X62345; CAA44218.1; -.
CC DR HSSP; P08631; 1BU1.
CC DR InterPro; IPR000719; Euk_pkinase.
CC DR InterPro; IPR000980; SH2.
CC DR InterPro; IPR001452; SH3.
CC DR InterPro; IPR001245; Tyr_pkinase.
CC DR Pfam; PF00017; SH2; 1.
CC DR Pfam; PF00018; SH3; 1.
CC DR Pfam; PF00069; pkinase; 1.
CC DR PRINTS; PR00401; SH2DOMAIN.
CC DR PRINTS; PR00452; SH3DOMAIN.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR ProDom; PD000001; Euk_pkinase; 1.
CC DR ProDom; PD000066; SH3; 1.
CC DR ProDom; PD000093; SH2; 1.
CC DR SMART; SM00252; SH2; 1.
CC DR SMART; SM00326; SH3; 1.
CC DR SMART; SM00219; TyrKc; 1.
CC DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
CC DR PROSITE; PS00109; PROTEIN KINASE TYR; 1.
CC DR PROSITE; PS50011; PROTEIN KINASE_DOM; 1.
CC DR PROSITE; PS50001; SH2; 1.
CC DR PROSITE; PS50002; SH3; 1.
CC KW Tyrosine-protein kinase; Phosphorylation; ATP-binding;
CC MYristate; SH2 domain; SH3 domain.
CC FT DOMAIN 55 115 SH3.
CC FT DOMAIN 121 218 SH2.
CC FT DOMAIN 239 492 PROTEIN KINASE.
CC FT NP_BIND 245 253 ATP (BY SIMILARITY).
CC FT BINDING 267 267 ATP (BY SIMILARITY).
CC FT ACT SITE 358 358 BY SIMILARITY.
CC FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
CC FT MOD RES 388 388 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC FT CONFLICT 51 51 F -> V (IN REF. 2).
CC FT CONFLICT 205 205 K -> R (IN REF. 2).
CC FT CONFLICT 306 306 I -> T (IN REF. 2).
CC SQ SEQUENCE 503 AA; 57016 MW; A1FC1F3F0B82FE73 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 503;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GSYSLSVR 135
Db 155 GSYSLSVR 162

RESULT 13
HCK_MACFA
ID ID_HCK_MACFA STANDARD; PRT; 504 AA.
AC Q95M30;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK) (Hemopoietic cell
DE kinase).
DE GN HCK.
```

OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC Cercopithecinae; Macaca.
 CC NCBI_TaxID=9541;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Picard C.;
 RL Theis (2001), University of Marseille, France.
 CC - FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE PC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS (BY SIMILARITY).
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC - SUBCELLULAR LOCATION: Membrane-associated (By similarity).
 CC - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL: A1320181; CAC44031.1; -.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 DR Transferrase: Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain.
 FT DOMAIN 56 116
 FT DOMAIN 122 219
 FT NP_BIND 240 493
 FT NP_BIND 246 254
 FT BINDING 268 268
 FT ACT_SITE 359 359
 FT LIPID 2 2
 FT MOD_RES 389 389
 FT SEQUENCE 504 AA; 57096 MW; 53B29322D2DE3423 CRC64;
 SO

Query Match 3.1%; Score 8; DB 1; Length 504;
 Best Local Similarity 100.0%; Pred. No. 7.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Gy 128 GSYSLSVR 135
 Db 156 GSYSLSVR 163

RESULT 14
 ID_LCK_CHICK STANDARD; PRT; 507 AA.
 AC P42683;
 DT 01-NOV-1995 (rel. 32, Created)
 DT 01-NOV-1995 (rel. 32, Last sequence update)
 DT 13-JUN-2002 (rel. 41, Last annotation update)

DE Proto-oncogene tyrosine-protein kinase LCK (EC 2.7.1.112) (Protein-
 DE tyrosine kinase C-TKL).
 GN LCK.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE OF 1-88 FROM N.A.
 RA MEDLINE=92186854; PubMed=1545804;
 RA Chow L., Ratcliffe M., Veilleux A.;
 RT "Lck is the avian homolog of the mammalian lck tyrosine protein
 RT kinase gene."
 RT Mol. Cell. Biol. 12:1226-1233 (1992).
 RL [2]
 RP SEQUENCE OF 46-507 FROM N.A.
 RA MEDLINE=88097370; PubMed=3321053;
 RA Streibhardt K., Mullins J.I., Bruck C., Ruebsamen-Waigmann H.;
 RT "Additional member of the protein-tyrosine kinase family: the src-
 RT and lck-related protooncogene c-tyl."
 RT Proc. Natl. Acad. Sci. U.S.A. 84:8778-8782 (1987).
 CC - FUNCTION: MAY PARTICIPATE IN ANTIGEN-INDUCED T-CELL ACTIVATION.
 CC - CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC - SUBCELLULAR LOCATION: BOUND TO THE CYTOPLASMIC DOMAIN OF EITHER
 CC CD4 OR CD8.
 CC - SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC - SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC - SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M85043; AAA49003.1; -.
 DR EMBL: J03579; AAA49081.1; ALU_INIT.
 DR HSP: P06239; LCK.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR001452; SH2.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYR_KC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation; Transferrase;
 KW ATP-binding; Myristate; SH2 domain; SH3 domain; Palmitate;
 KW Lipo-protein.
 FT INIT_MET 0 0
 FT LIPID 1 1
 FT LIPID 2 2
 FT LIPID 4 4
 FT DOMAIN 59 119
 FT DOMAIN 125 222
 FT SH2.

FT DOMAIN 243 496 PROTEIN KINASE.
 FT NP_BIND 249 257 ATP (BY SIMILARITY).
 FT BINDING 271 271 ATP (BY SIMILARITY).
 FT ACT_SITE 362 362 BY SIMILARITY.
 FT MOD_RES 392 392 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 503 503 PHOSPHORYLATION (NEGATIVE REGULATION) (BY SIMILARITY).
 SQ SEQUENCE 507 AA; 58008 MW; BC83C4FA9136170 CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 8; DB 1; Length 507;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 128 GSYSLSVR 135
 Db 159 GSYSLSVR 166
 RESULT 15
 LYN_HUMAN STANDARD; PRT; 511 AA.
 AC P07948;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8712710; PubMed=3561390;
 RA Yananishi Y., Fukushima S.-I., Samba K., Sukegawa J., Miyajima N.,
 RA Matsubara K.-I., Yamamoto T., Toyoshima K.;
 RT "The yee-related cellular gene lyn encodes a possible tyrosine kinase
 RT similar to p56lck.";
 RL Mol. Cell. Biol. 7:237-243 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94171041; PubMed=8125304;
 RA Rider L.G., Raben N., Miller L., Jelsema C.;
 RT "The cdnas encoding two forms of the lyn protein tyrosine kinase are
 RT expressed in rat mast cells and human myeloid cells.";
 RL Gene 138:219-222 (1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; M16038; AAA59540.1; -;
 DR EMBL; M79321; AAB50019.1; -;
 DR PIR; A26719; TYHULY.
 DR HSPSP; P08631; 1A05.
 DR Genew; HGNC:6735; LYN.
 DR MIM; 165120; -;
 DR Interpro; IPR000719; Euk_pkinase.
 DR Interpro; IPR000980; SH2.
 DR Interpro; IPR001452; SH3.
 DR Interpro; IPR001245; Tyr_pkinase.

DR Pfam; PF00017; SH2; 1.
 DR Pfam; PF00018; SH3; 1.
 DR Pfam; PF00069; kinase; 1.
 DR PRINTS; PR00452; SH2DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Euk_pkinase.
 DR PRODOM; PD000066; SH3; 1.
 DR PRODOM; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT MET 0
 FT LIPID 1 1
 FT LIPID 2 2
 FT DOMAIN 62 122
 FT DOMAIN 128 225
 FT DOMAIN 246 500
 FT NP_BIND 252 260
 FT BINDING 274 274
 FT ACT_SITE 366 366
 FT MOD_RES 396 396
 FT MOD_RES 507 507
 FT VARSPES 42
 SQ SEQUENCE 511 AA; 58442 MW; 8419CD461204E364 CRC64;
 Query Match
 Best Local Similarity 100.0%; Score 8; DB 1; Length 511;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 116 GAFLRES 123
 Db 150 GAFLRES 157
 RESULT 16
 LYN_MOUSE STANDARD; PRT; 511 AA.
 ID LYN_MOUSE
 AC P25911; 062127;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Scurionath; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91260688; PubMed=1710766;
 RA Stanley E., Ralph S.J., McEwen S., Boulet I., Holtzman D.A.,
 RA Lock P., Dunn A.R.;
 RT "Alternatively spliced murine lyn mRNAs encode distinct proteins.";
 RL Mol. Cell. Biol. 11:3399-3406 (1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91203857; PubMed=2017160;
 RA Yi T., Boien J.B., Ihle J.N.;
 RT "Hematopoietic cells express two forms of lyn kinase differing by 21
 RT amino acids in the amino terminus.";
 RL Mol. Cell. Biol. 11:2391-2398 (1991).
 RN [3]
 RP SEQUENCE OF 363-431 FROM N.A.
 RX MEDLINE=90152381; PubMed=2482828;
 RA Wilks A.F., Kurban R.R., Hovens C.M., Ralph S.J.;

RT "The application of the polymerase chain reaction to cloning members
 RT of the protein tyrosine kinase family.";
 RT Gene 85:67-74(1989)
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL, M64608; AAA39470.1; -;
 DR EMBL, M57696; AAA39471.1; -;
 DR EMBL, M57697; AAA39472.1; -;
 DR EMBL, M33426; AAA40017.1; -;
 DR PIR, A39719; A39719.
 DR HSSP, P08631; 1AD5.
 DR MGD, MGI:96892; LYN.
 DR InterPro, IPR000719; Euk_pkinase.
 DR InterPro, IPR000980; SH2.
 DR InterPro, IPR001452; SH3.
 DR InterPro, IPR001245; Tyr_pkinase.
 DR Pfam, PF00017; SH2; 1.
 DR Pfam, PF00018; SH3; 1.
 DR Pfam, PF00069; pkinase; 1.
 DR PRINTS, PR00452; SH3DOMAIN.
 DR PRINTS, PR00109; TYRKINASE.
 DR ProDom, PD000001; Euk_pkinase; 1.
 DR ProDom, PD000066; SH3; 1.
 DR ProDom, PD000093; SH2; 1.
 DR SMART, SMO0252; SH2; 1.
 DR SMART, SMO0326; SH3; 1.
 DR SMART, SMO0219; Tyrc; 1.
 DR PROSITE, PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE, PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE, PS00111; PROTEIN_KINASE_DOM; 1.
 DR PROSITE, PS50002; SH3; 1.
 DR PROSITE, PS50001; SH2; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Wristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 KW INIT MET
 FT INIT MET 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH2.
 FT DOMAIN 246 500 PROTEIN KINASE.
 FT NP BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT SITE 366 366 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 396 396 PHOSPHORYLATION (BY SIMILARITY).
 FT MOD_RES 507 507 MISSING (IN ISOFORM LYN B).
 FT VARSPPLIC 24 44 MISSING (IN ISOFORM LYN B).
 FT CONFLICT 76 76 I -> F (IN REF. 2).
 FT CONFLICT 160 160 L -> I (IN REF. 2).
 FT CONFLICT 278 278 P -> L (IN REF. 2).
 FT CONFLICT 390 390 V -> I (IN REF. 2).
 FT CONFLICT 414 414 I -> F (IN REF. 3).
 FT CONFLICT 424 424 D -> N (IN REF. 1).
 FT CONFLICT 431 431 L -> P (IN REF. 3).
 FT CONFLICT 431 431
 SQ SEQUENCE 511 AA; 58681 MW; 3935221CC90C50F0 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 511;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 116 GAFLIRS 123
 DB 150 GAFLIRS 157
 RESULT 17
 LYN_RAT
 ID LYN_RAT STANDARD; PRT; 511 AA.
 AC 007014; 063320;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase LYN (EC 2.7.1.112).
 GN LYN.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_Taxid=10116;
 OX [1]
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Winochuk K., Nishikata H., Stragani R.P.;
 RT "Bacterially expressed rat p56lyn binds several proteins in rat
 RT basophilic leukemia cells including pp72, a tyrosine phosphorylated
 RT protein prominent in activated cells.";
 RL J. Immunol. 150:222-222(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=9417041; PubMed=8125304;
 RA Ridg L.G., Raben N., Miller L., Jalsena C.;
 RT "The cDNAs encoding two forms of the LYN protein tyrosine kinase are
 RT expressed in rat mast cells and human myeloid cells.";
 RL Gene 138:219-222(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97442484; PubMed=9295361;
 RX Vonakis B.M., Chen H., Haleem-Smith H., Metzger H.;
 RT "The unique domain as the site on LYN kinase for its constitutive
 RT association with the high affinity receptor for Ige.";
 RL J. Biol. Chem. 272:24072-24080(1997).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS, LYN A (SHOWN HERE) AND LYN B;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN B-LYMPHOID AND
 CC MYELOID CELLS.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL, L14951; AAA41549.1; -;
 DR EMBL, L14782; AAA20944.1; -;
 DR EMBL, L14823; AAA20945.1; -;
 DR EMBL, AF000300; AAB71344.1; -;
 DR EMBL, AF000301; AAB71345.1; -;
 DR EMBL, AF000302; AAB71346.1; -;
 DR HSSP, P08631; 1AD5.
 DR InterPro, IPR000719; Euk_pkinase.
 DR InterPro, IPR000980; SH2.
 DR InterPro, IPR001452; SH3.
 DR InterPro, IPR001245; Tyr_pkinase.

DR Pfam; PR00017; SH2; 1.
 DR Pfam; PR00018; SH3; 1.
 DR Pfam; PR00069; PKINASE; 1.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk PKINASE; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
 KW Transferase; ATP-binding; Myristate; SH2 domain; SH3 domain;
 KW Palmitate; Lipoprotein; Alternative splicing.
 FT INIT_MET 0 0
 FT LIPID 1 1 MYRISTATE (BY SIMILARITY).
 FT LIPID 2 2 PALMITATE (BY SIMILARITY).
 FT DOMAIN 62 122 SH3.
 FT DOMAIN 128 225 SH3.
 FT DOMAIN 245 500 PROTEIN_KINASE.
 FT NP_BIND 252 260 ATP (BY SIMILARITY).
 FT BINDING 274 274 ATP (BY SIMILARITY).
 FT ACT_SITE 366 366 ATP (BY SIMILARITY).
 FT MOD_RES 396 396 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 507 507 PHOSPHORYLATION (BY SIMILARITY).
 FT VARSPLIC 24 44 MISSING (IN ISOFORM LYN B).
 FT CONFLICT 230 230 P -> L (IN REF. 2).
 FT CONFLICT 307 307 V -> A (IN REF. 2).
 FT CONFLICT 418 418 C -> Y (IN REF. 2).
 SQ SEQUENCE 511 AA; 58529 MW; 24A2E5E229CD3ED CRC64;

Query Match 3.1%; Score 8; DB 1; Length 511;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR 116 GAFIIRS 123
 DB 150 GAFIIRS 157

RESULT 18
 ID FGR_MOUSE STANDARD; PRT; 517 AA.
 AC P14234; O61404;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Proto-oncogene tyrosine-protein kinase FGR (EC 2.7.1.112) (P55-FGR)
 DE (C-FGR).
 GN FGR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA/20;
 RX MEDLINE=89385605; PubMed=2674853;
 RA Y1 T.L., Willman C.L.;
 RT Cloning of the murine c-fgr proto-oncogene cDNA and induction of
 RT c-fgr expression by proliferation and activation factors in normal
 RT bone marrow-derived monocytic cells.;
 RL Oncogene 4:1081-1087 (1989).
 RU [2]
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Monocytic leukemia;
 RX MEDLINE=90191719; PubMed=2179817;
 RA King F.J., Cole M.D.;

RT "Molecular Cloning and sequencing of the murine c-fgr gene";
 RL Oncogene 5:337-344 (1990)
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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 CC -----
 DR EMBL; X16440; CAA34463.1; -;
 DR EMBL; X52191; CAA36437.1; -;
 DR PIR; A33127; A33127.
 DR PIR; S10072; S10072.
 DR HSSP; P00523; 2PTK.
 DR MCD; MGI.95527; Fgr.
 DR InterPro; IPR000719; Euk PKINASE.
 DR InterPro; IPR000980; SH2.
 DR InterPro; IPR001452; SH3.
 DR InterPro; IPR001245; Tyr PKINASE.
 DR Pfam; PR00017; SH2; 1.
 DR Pfam; PR00018; SH3; 1.
 DR Pfam; PR00069; PKINASE; 1.
 DR PRINTS; PR00401; SH3DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Euk PKINASE; 1.
 DR ProDom; PD000066; SH3; 1.
 DR ProDom; PD000093; SH2; 1.
 DR SMART; SM00252; SH2; 1.
 DR SMART; SM00326; SH3; 1.
 DR SMART; SM00219; TYRc; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 1.
 DR PROSITE; PS50002; SH3; 1.
 KW Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
 KW Phosphorylation; SH2 domain; SH3 domain.
 FT DOMAIN 65 126 SH3.
 FT DOMAIN 132 229 SH2.
 FT DOMAIN 251 504 PROTEIN_KINASE.
 FT NP_BIND 257 265 ATP (BY SIMILARITY).
 FT BINDING 279 279 ATP (BY SIMILARITY).
 FT ACT_SITE 370 370 BY SIMILARITY.
 FT MOD_RES 400 400 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT MOD_RES 418 418 N -> T (IN REF. 2).
 FT CONFLICT 41 41 Q -> R (IN REF. 2).
 FT CONFLICT 212 212
 SQ SEQUENCE 517 AA; 58867 MW; F655BDB4510F3076 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 517;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DR 116 GAFIIRS 123
 DB 154 GAFIIRS 161

RESULT 19
 ID HCK_MOUSE STANDARD; PRT; 524 AA.
 AC F08103;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P56-HCK and P60-HCK)
 DE (Hemopoietic cell kinase) (B-cell/myeloid kinase) (BMK).
 GN HCK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OK NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE OF 22-524 FROM N.A.
 RC STRAIN=ICR; TISSUE=Macrophage;
 RX MEDLINE=88067781; PubMed=3684607;
 RA Klemes M.J., McKecher S.R., Maki R.A.;
 RL "Nucleotide sequence of the mouse hck gene";
 RT Nucleic Acids Res. 15:9600-9600(1987).
 RN [2]
 RP SEQUENCE OF 22-524 FROM N.A.
 RX MEDLINE=88068587; PubMed=3317404;
 RA Holtzman D.A., Cook W.D., Dunn A.R.;
 RT "Isolation and sequence of a cDNA corresponding to a src-related gene
 RT expressed in murine hemopoietic cells";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:8325-8329(1987).
 RN [3]
 RP SEQUENCE OF 1-22 FROM N.A., AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization";
 RL Mol. Cell. Biol. 11:4363-4370(1991).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P59-HCK AND P56-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P59-HCK IS ALSO CYTOPLASMIC.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, 1P59-HCK (shown here) and P56-
 CC HCK: are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
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DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; Tyrc; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Transferase; Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Myristate; SH2 domain; SH3 domain; Alternative initiation.
 FT CHAIN 1 524 TYROSINE-PROTEIN KINASE P59-HCK.
 FT INIT MET 22 524 TYROSINE-PROTEIN KINASE P56-HCK.
 FT DOMAIN 142 239 SH2.
 FT DOMAIN 260 513 SH3.
 FT NP BIND 266 274 ATP (BY SIMILARITY).
 FT BINDING 288 288 ATP (BY SIMILARITY).
 FT ACT SITE 379 379 BY SIMILARITY.
 FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
 FT MOD RES 409 409 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SO SEQUENCE 524 AA; 59129 MW; D672ED59B38C9706 CRC64;
 Qy 128 GSYSLSVR 135 3.1%; Score 8; DB 1; Length 524;
 Db 176 GSYSLSVR 183 Best Local Similarity 100.0%; Pred. No. 7.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 20
 HCK_HUMAN STANDARD; PRT: 526 AA.
 ID HCK_HUMAN
 AC P08631; O96CC0; O9H5Y5; O9NU4; O9NUM5;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tyrosine-protein kinase HCK (EC 2.7.1.112) (P59-HCK and P60-HCK)
 DE (Hemopoietic cell kinase).
 GN HCK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX MEDLINE=87257942; PubMed=3496523;
 RA Quinirell N., Lebo R., Varnus H., Bishop J.M., Pettenati M.J.,
 RA le Beau M.M., Diaz M.O., Rowley J.D.;
 RT "Identification of a human gene (hck) that encodes a protein-tyrosine
 RT kinase and is expressed in hemopoietic cells";
 RL Mol. Cell. Biol. 7:2267-2275(1987).
 RN [2]
 RP SEQUENCE OF 22-526 FROM N.A.
 RX MEDLINE=87257943; PubMed=3453117;
 RA Ziegler S.F., Marth J.D., Lewis D.B., Perlmuter R.M.;
 RT "Novel protein-tyrosine kinase gene (hck) preferentially expressed in
 RT cells of hemopoietic origin";
 RL Mol. Cell. Biol. 7:2276-2285(1987).
 RN [3]
 RP SEQUENCE OF 22-526 FROM N.A.
 RC TISSUE=B-cell;
 RA Strausberg R.;
 RN Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 22-526 FROM N.A.
 RC TISSUE=ileal mucosa;
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga W., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hiro M., Ohmori Y., Ota T., Suzuki Y.,

RA Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Itozai T., Sugano S.; "NEBO human cDNA sequencing project."
 RT Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavris G., Almeida J.P., Babbage A.K., Bagguley C.L.,
 RA Bailey J., Barlow K.P., Bates K.N., Beard L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Burrill W.D., Butler A.P., Gardner C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.,
 RA Ballington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekesch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Leharasalo M.H., Leversha W.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McCormachie L.J., McLeay K., McMurray A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Rose M.T., Scott C.E., Sehra H.K., Shomkhen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Symmore N., Taylor R., Tee U., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M., Thorne P.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Dublin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20."
 RL Nature 414:865-871 (2001).
 RN [6]
 RP SEQUENCE OF 179-526 FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=92241680; PubMed=1572549;
 RA Hradetzky D., Strebhardt K., Ruebsamen-Waigmann H.;
 RT "The genomic locus of the human hemopoietic-specific cell protein
 RT tyrosine kinase (PTK)-encoding gene (HCK) confirms conservation of
 RT exon-intron structure among human PTKs of the src family.";
 RL Gene 113:275-280 (1992).
 RN [7]
 RP SEQUENCE OF 1-22 FROM N.A. AND ALTERNATIVE INITIATION.
 RX MEDLINE=91342636; PubMed=1875927;
 RA Lock P., Ralph S., Stanley E., Boulet I., Ramsay R., Dunn A.R.;
 RT "Two isoforms of murine hck, generated by utilization of alternative
 RT translational initiation codons, exhibit different patterns of
 RT subcellular localization.";
 RL Mol. Cell. Biol. 11:4363-4370 (1991).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 78-526.
 RX MEDLINE=97177106; PubMed=9024658;
 RA Sichert F., Moarrefi I., Kuriyan J.;
 RT "Crystal structure of the Src family tyrosine kinase Hck.";
 RL Nature 385:602-609 (1997).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 81-137.
 RX MEDLINE=98453315; PubMed=9778343;
 RA Arold S., O'Brien R., Franken P., Strub M.P., Hoh F., Dumas C.,
 RA Ladbury J.E.;
 RT "RT loop flexibility enhances the specificity of Src family SH3
 RT domains for HIV-1 Nef.";
 RL Biochemistry 37:14683-14691 (1998).
 RN [10]
 RP STRUCTURE BY NMR OF 78-138.
 RX MEDLINE=98239731; PubMed=9571048;
 RA Morita D.A., Baldasseri D.M., Zhang W., Altieri A.S., Smithgall T.E.,
 RA Smeiter W.H., Byrd R.A.;
 RT "Solution structure of the human Hck SH3 domain and identification of
 RT its ligand binding site.";
 RL J. Mol. Biol. 278:253-265 (1998).

RN [11]
 RP STRUCTURE BY NMR OF 139-245.
 RX MEDLINE=97263487; PubMed=9109402;
 RA Zhang W., Smithgall T.E., Smeiter W.H.;
 RT "Sequential assignment and secondary structure determination for the
 RT Src homology 2 domain of hematopoietic cellular kinase.";
 RL FEBS Lett. 406:131-135 (1997).
 CC -1- FUNCTION: MAY SERVE AS PART OF A SIGNALING PATHWAY COUPLING THE FC
 CC RECEPTOR TO THE ACTIVATION OF THE RESPIRATORY BURST. MAY ALSO
 CC CONTRIBUTE TO NEUTROPHIL MIGRATION AND MAY REGULATE THE
 CC DEGRANULATION PROCESS OF NEUTROPHILS.
 CC CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBCELLULAR LOCATION: P60-HCK AND P59-HCK ARE ASSOCIATED WITH
 CC MEMBRANES. P60-HCK IS ALSO CYTOPLASMIC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; P60-HCK (shown here) and P59-
 CC HCK; are produced by alternative initiation.
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CELLS OF THE
 CC MYELOID AND B-LYMPHOID LINEAGES.
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M16591; AAA52643.1; -;
 DR EMBL: M16592; AAA52644.1; -;
 DR EMBL: BC014435; AAH14435.1; -;
 DR EMBL: AK026432; BAB15482.1; -;
 DR EMBL: AL049533; CAB75606.1; -;
 DR EMBL: X58741; CAA1565.2; -;
 DR EMBL: X58742; CAA1565.2; JOINED.
 DR EMBL: X58743; CAA1565.2; JOINED.
 DR PIR: A27812; TVH0HC.
 DR PDB: 2HCK; 20-AUG-97.
 DR PDB: 3HCK; 15-OCT-97.
 DR PDB: 4HCK; 17-JUN-98.
 DR PDB: 5HCK; 17-JUN-98.
 DR PDB: 1AD5; 15-MAY-97.
 DR PDB: 1BUL; 11-NOV-98.
 DR Genew: HGNC:4840; HCK.
 DR MIM: 142370; -;
 DR Interpro: IPR000719; Euk_pkinase.
 DR Interpro: IPR000980; SH2.
 DR Interpro: IPR001452; SH3.
 DR Interpro: IPR002290; Ser_thr_pkinase.
 DR Interpro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 2.
 DR Pfam: PF00069; pkinase; 4.
 DR Prodom: PD000066; SH3; 1.
 DR Prodom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00329; SH3; 1.
 DR SMART: SM00220; S_TKC; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PSS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PSS0002; SH3; 1.
 KW Transferase: Tyrosine-protein kinase; Phosphorylation; ATP-binding;
 KW Myristate: SH2 domain; SH3 domain; Alternative initiation;
 KW 3D-structure: 1 526 TYROSINE-PROTEIN KINASE P60-HCK.
 FT CHAIN 22 526 TYROSINE-PROTEIN KINASE P59-HCK.


```

CC INIT MET 22 22 FOR ISOFORM P59-HCK.
CC FT DOMAIN 78 138 SH3.
CC FT DOMAIN 144 241 SH2.
CC FT DOMAIN 262 515 PROTEIN KINASE.
CC FT NP_BIND 268 276 ATP.
CC FT BINDING 290 290 ATP.
CC FT ACT SITE 381 381 MYRISTATE (BY SIMILARITY).
CC FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
CC FT LIPID 23 23 MYRISTATE (BY SIMILARITY).
CC FT MOD_RES 411 411 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC FT CONFLICT 24 24 C -> S (IN REF. 1).
CC FT CONFLICT 144 144 W -> R (IN REF. 4).
CC FT SEQUENCE 526 AA, 59599 MW, 847877A0A641725 CRC64;

Query Match 3.1%; Score 8; DB 1; Length 526;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 128 GSYSLSVR 135
DB 178 GSYSLSVR 185

RESULT 21
FGR_HUMAN STANDARD; PRT; 529 AA.
AC P09769;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-JUN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase fgr (BC 2.7.1.112) (P55-FGR)
DE (C-FGR).
DE FGR OR SRC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=8094395; PubMed=3275868;
RA Katamine S., Notario V., Rao C.D., Miki T., Cheah M.S.C.,
RT Tronick S.R., Robbins K.C.;
RL Mol. Cell. Biol. 8:259-266(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA Heath P.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymph;
RA Straubeberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 111-416 FROM N.A.
RX MEDLINE=8706434; PubMed=3023853;
RA Nishizawa M., Semba K., Yoshida M.C., Yamamoto T., Sasaki M.,
RA Toyoshima K.;
RT "Structure, expression, and chromosomal location of the human c-fgr
RT gene";
RL Mol. Cell. Biol. 6:511-517(1986).
RN [5]
RP SEQUENCE OF 1-143 FROM N.A.
RX MEDLINE=8826220; PubMed=3330776;
RA Inoue K., Ikawa S., Semba K., Sukegawa J., Yamamoto T., Toyoshima K.;
RT "Isolation and sequencing of cDNA clones homologous to the v-fgr
RT oncogene from a human B lymphocyte cell line, IM-9.";
RL Oncogene 1:301-304(1987).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC : tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.

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CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M19722; AA55451.1; -.
CC EMBL: AL031729; CAB62988.1; -.
CC EMBL: BC002836; AA02836.1; -.
CC EMBL: M12724; AA55762.1; JOINED.
CC EMBL: M12719; AA55762.1; JOINED.
CC EMBL: M12720; AA55762.1; JOINED.
CC EMBL: M12721; AA55762.1; JOINED.
CC EMBL: M12722; AA55762.1; JOINED.
CC EMBL: M12723; AA55762.1; JOINED.
CC PIR: A27676; TYRUP..
CC PIR: A28353; A28353.
CC HSP: P06241; ISHF.
CC Genew: HGNC:3697; FGR.
CC MIM: 164940; -.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR000980; SH2.
CC InterPro: IPR001452; SH3.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00017; SH2_1.
CC Pfam: PF00018; SH3_1.
CC Pfam: PF00069; pkinase_1.
CC PRINTS: PR00401; SH2DOMAIN.
CC PRINTS: PR00452; SH3DOMAIN.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Euk_pkinase_1.
CC ProDom: PD000066; SH3_1.
CC ProDom: PD000093; SH2_1.
CC SMART: SM00252; SH2; 1.
CC SMART: SM00326; SH3; 1.
CC SMART: SM00219; TyKc; 1.
CC PROSITE: PS00107; PROTEIN KINASE ATP; 1.
CC PROSITE: PS00109; PROTEIN KINASE TYR; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS50001; SH2; 1.
CC PROSITE: PS50002; SH3; 1.
CC Kx Transferrase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
CC Km Phosphorylation; SH2 domain; SH3 domain.
CC FT DOMAIN 77 138 SH2.
CC FT DOMAIN 144 241 SH3.
CC FT DOMAIN 263 516 PROTEIN KINASE.
CC FT NP_BIND 269 277 ATP (BY SIMILARITY).
CC FT BINDING 291 291 ATP (BY SIMILARITY).
CC FT ACT SITE 382 382 BY SIMILARITY.
CC FT MOD_RES 412 412 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
CC SEQUENCE 529 AA; 59478 MW; 688C1E08414E0F9C CRC64;

Query Match 3.1%; Score 8; DB 1; Length 529;
Best Local Similarity 100.0%; Pred. No. 7.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 116 GAFILRES 123
DB 166 GAFILRES 173

RESULT 22
FYN_MOUSE STANDARD; PRT; 533 AA.
AC P39688;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase fyn (EC 2.7.1.112) (P59-FYN).

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GN FYN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91175680; PubMed=2488273;
 RA Cooke M.P., Perlmuter R.M.;
 RT "Expression of a novel form of the fyn proto-oncogene in
 RT hematopoietic cells";
 RL New Biol. 1:66-74(1989).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Lee C., Kim M.G., Jeon S.H., Park D.E., Park S.D., Seong R.H.;
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
 RN (3)
 RP PALMITOYLATION.
 RX MEDLINE=94019312; PubMed=8413337;
 RA Shenoy-Scaria A.M., Timson L.K., Kwong J., Shaw A.S., Lublin D.M.;
 RT "Palmitoylation of an amino-terminal cysteine motif of protein
 RT tyrosine kinases p56lck and p59fyn mediates interaction with
 RT glycosyl-phosphatidylinositol-anchored proteins";
 RL Mol. Cell. Biol. 13:6385-6392(1993).
 RN (4)
 RP PALMITOYLATION.
 RX MEDLINE=95071286; PubMed=7980442;
 RA Koegl M., Zlatkine P., Ley S.C., Courtneidge S.A., Magee A.T.;
 RT "Palmitoylation of multiple Src-family kinases at a homologous N-
 RT terminal motif";
 RL Biochem. J. 303:749-753(1994).
 RN (5)
 RP PALMITOYLATION.
 RX MEDLINE=97345356; PubMed=9201723;
 RA Wolven A., Okamura H., Rosenblatt Y., Reeh M.D.;
 RT "Palmitoylation of p59fyn is reversible and sufficient for plasma
 RT membrane association";
 RL Mol. Biol. Cell 8:1159-1173(1997).
 RN (6)
 RP MYRISTOYLATION.
 RX MEDLINE=96251668; PubMed=8655574;
 RA Gauen L.K.T., Linder M.E., Shew A.S.;
 RT "Multiple features of the p59fyn src homology 4 domain define a motif
 RT for immune-receptor tyrosine-based activation motif (ITAM) binding
 RT and for plasma membrane localization";
 RL J. Cell Biol. 133:1007-1015(1996).
 CC -1- FUNCTION: IMPLICATED IN THE CONTROL OF CELL GROWTH.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: ASSOCIATES THROUGH ITS SH3 DOMAIN, TO THE P85 SUBUNIT OF
 CC PHOSPHATIDYLINOSITOL 3-KINASE. INTERACTS WITH THE FYN-BINDING
 CC PROTEIN (FVB)
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
 CC SUBFAMILY.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
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 CC -----
 DR EMBL: M27266; AAA37644.1; -;
 DR EMBL: U70324; AAB09568.1; -;
 DR PIR: A44991; A44991.
 DR HSP: P06241; 1PYN.
 DR MGI: MGI:95602; FYN.
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR000980; SH2.
 DR InterPro: IPR001452; SH3.

DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00017; SH2; 1.
 DR Pfam: PF00018; SH3; 1.
 DR Pfam: PF00069; pkinase; 1.
 DR PRINTS: PR00401; SH2DOMAIN.
 DR PRINTS: PR00452; SH3DOMAIN.
 DR PRINTS: PR00109; TYRKINASE.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR ProDom: PD000066; SH3; 1.
 DR ProDom: PD000093; SH2; 1.
 DR SMART: SM00252; SH2; 1.
 DR SMART: SM00326; SH3; 1.
 DR SMART: SM00219; TYRK; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE: PS50001; SH2; 1.
 DR PROSITE: PS50002; SH3; 1.
 KW Proto-oncogene; transferase; Tyrosine-protein kinase; phosphorylation;
 KW ATP-binding; myristate; SH3 domain; SH2 domain; palmitate;
 KW Lipoprotein.
 FT INIT MET 0 0
 FT LIPID 1 1
 FT LIPID 2 2
 FT LIPID 5 5
 FT LIPID 142 142
 FT DOMAIN 148 245
 FT DOMAIN 267 520
 FT NP_BIND 273 281
 FT BINDING 295 295
 FT ACT_SITE 386 386
 FT MOD_RES 416 416
 FT SEQUENCE 533 AA; 59926 MW; EFPD703F15B2933C CRC64;
 Query Match 3 1%; Score 8; DB 1; Length 533;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 118 FLIRESGT 125
 DB 172 FLIRESGT 179
 RESULT 23
 GCPE_HUMAN STANDARD; PRT; 1819 AA.
 ID GCPE_HUMAN
 AC Q96RT7; Q9BY91; Q9UGX3; Q9UGX4;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Gamma-tubulin complex component 6 (GCPE-6).
 GN GCPE OR KIA1669.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RX MEDLINE=21551508; PubMed=1164571.
 RA Murphy S.M., Preble A.M., Patel U.K., O'Connell K.L., Dias D.P.,
 RA Moritz W., Agard D., Stules J.T., Stearns T.;
 RT "GCPE and GCPE6: two new members of the human gamma-tubulin complex";
 RL Mol. Biol. Cell 12:3340-3352(2001).
 RN (2)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Brunklewich R., Beare D.M.,
 RA Clamp M., Smith L.J., Atencough R., Almeida J.P., Babbage A.K.,
 RA Baguley C., Bailey U., Bartlow K.F., Bates K.N., Beasly O.P.,
 RA Bird C.P., Blakey S.E., Bridgman A.W., Buck D., Burgess J.,
 RA Burrill M.D., Burton J., Carter C., Carter N.P., Chen Y., Clark G.,
 RA Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R.,
 RA Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E.,

RA Dhami P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G.,
RA Evans K.L., Fey J.M., Fleming K., French L., Garner A.A.,
RA Gilbert J.G.R., Goward M.E., Heatham D.V., Griffiths M.N.D., Hall C.,
RA Hall R.E., Hall-Tamlyn G., Heathcote R.W., Ho S., Holmes S.,
RA Hunt S.E., Jones M.C., Kersey J., Kimberley A.M., King A.,
RA Laird G.K., Langford C.F., Leverisha M.A., Lloyd C., Lloyd D.M.,
RA Martyn I.D., Mashreghi-Mohammadi M., Matthews L.H., Mcann O.T.,
RA Mcleay J., McLaren S., McMurray A.A., Milne S.A., Mortimore B.J.,
RA Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T.,
RA Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T.,
RA Scott C.E., Sehra H.K., Skuce C.D., Smalley S., Smith M.L.,
RA Soderlund C., Spragon L., Steward C.A., Stilson J.E., Swann R.M.,
RA Vaden M., Wall M., Wallis J.M., Whiteley W.N., Willey D.L.,
RA Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L.,
RA Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N.,
RA Mnoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J.,
RA Shintant A., Shibuya K., Yoshitaki Y., Aoki N., Mitsuyama S.,
RA Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T.,
RA Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I.,
RA Lewis J., Lewis S., Lin S.-P., Lon P., Malaj E., Nguyen T., Pan H.,
RA Phan S., Qi S., Qian Y., Ray L., Ren Q., Shaull S., Sloan D., Song L.,
RA Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z.,
RA Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Minx P.,
RA Fulton R., Johnson D., Bemis G., Bentley D., Bradsheaw H., Bourne S.,
RA Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J.,
RA Hinde K., Kemp K., Latreille P., Layman D., Ozerky P., Rohlfing T.,
RA Schest P., Walker C., Mansley A., Wohlmann P., Popin K., Nelson J.,
RA Korf I., Bedell J.A., Hillier L., Martis E., Waterston R., Wilson R.,
RA Emanuel B.S., Shaikh T., Kurahashi H., Salter S., Budarf M.L.,
RA McDermid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L.,
RA Kim U.J., Shizuya H., Simon M.I., Dumanski J.P., Peyraud M., Kedra D.,
RA Seroussi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P.,
RA Wilkinson P., Bodenreich A., Hartman K., Hu X., Khan A.S., Lane L.,
RA Tlajuhn Y., Wright H.,
RT "The DNA sequence of human chromosome 22.",
RL Mature 402:489-495(1999).
RN
RP SEQUENCE OF 33-1819 FROM N.A. (ISOFORM 2).
RC TISSUE=Brain;
RX MDLINE=21156230; PubMed=1258795;
RA Hiroawa M., Nagase T., Murahashi Y., Kikuno R., Ohara O.,
RT "Identification of novel transcribed sequences on human chromosome 22
RT by expressed sequence tag mapping.";
RL DNA Res. 8:1-9(2001).
CC
CC -1- FUNCTION: Gamma-tubulin complex is necessary for microtubule
CC nucleation at the centrosome.
CC -1- SUBUNIT: Gamma-tubulin complex is composed of gamma-tubulin, GCP2,
CC GCP3, GCP4, GCP5 and GCP6.
CC
CC -1- SUBCELLULAR LOCATION: Centrosome.
CC
CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
CC produced by alternative splicing.
CC
CC -1- SIMILARITY: BELONGS TO THE GCP FAMILY.
CC
CC -1- CAUTION: Ref 3 sequence differs from that shown due to frameshifts
CC in positions 1371 and 1758.
CC
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CC
CC
CC EMBL; AF272887; AAK82968.1; -;
CC EMBL; AL022328; CAB63046.1; ALT SEQ.
CC EMBL; AL022328; CAB63047.1; ALT SEQ.
CC EMBL; AB051456; BAB3339.1; ALT FRAME.
CC Microtubules; Repeat; Alternative splicing.
CC
CC DOMAIN 1027 1269 9 x 27 AA TANDDEM REPEATS.
CC REPEAT 1027 1053 1.
CC REPEAT 1054 1080 2.
CC REPEAT 1081 1107 3.
CC REPEAT 1108 1134 4.

FT REPEAT 1135 1161 5.
FT REPEAT 1162 1188 6.
FT REPEAT 1189 1215 7.
FT REPEAT 1216 1242 8.
FT REPEAT 1243 1269 9.
FT VARSPLIC 1724 1757 MISSING (IN ISOFORM 2).
FT CONFLICT 567 567 S -> L (IN REF. 3).
FT CONFLICT 1377 1377 A -> T (IN REF. 2 AND 3).
SQ CONFLICT 1621 1621 L -> V (IN REF. 2).
SQ SEQUENCE 1819 AA; 200455 MW; 92357654434594A CRC64;
Query Match 3.1%; Score 8; DB 1; Length 1819;
Best Local Similarity 100.0%; Pred No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 170 QALVDHYS 177
Db 758 QALVDHYS 765
RESULT 24
N511 SOYBN STANDARD; PRT; 137 AA.
ID N511 SOYBN
AC 005544;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Early nodulin 55-1 precursor (N-55-1) (Fragment).
GN ENOD55-1.
OS Glycine max (Soybean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX NCBI_TaxID=3847;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Williams; TISSUE=Root;
RX MEDLINE=94003074; PubMed=8400132;
RA de Blank C., Mylona P., Katinakis P.C., Biseling T., Franssen H.,
RT "Characterization of the soybean early nodulin cDNA clone GmENOD55.";
RL Plant Mol. Biol. 22:1167-1171(1993).
CC
CC -1- SUBCELLULAR LOCATION: PERIBACTEROID MEMBRANE (POTENTIAL).
CC
CC -1- DEVELOPMENTAL STAGE: EXPRESSED AT EARLY STAGES OF NODULE
CC DEVELOPMENT. MAXIMAL EXPRESSION IS SEEN IN NODULES FROM 14-DAY-OLD
CC PLANTS AFTER WHICH LEVELS DECREASE.
CC
CC -1- INDUCTION: DURING NODULATION IN LEGUME ROOTS AFTER RHIZOBIUM
CC INFECTION, AND AFTER RELEASE OF BACTERIA FROM THE INFECTION
CC THREAD.
CC
CC -1- SIMILARITY: CONTAINS 1 PLASTOCYANIN-LIKE DOMAIN.
CC
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CC
CC
CC EMBL; X69156; CAA48908.1; -;
CC InterPro: IPR003245; Pfam: PF002298; Cb bind like: 1.
CC Pfam: PF003122; P1cyanin like: 1.
CC Nodulation; Glycoprotein; Nitrogen fixation; Signal; Membrane.
CC
CC NON_TER 1 1
CC SIGNAL 1 1
CC CHAIN 1 137
CC DOMAIN 13 137
CC CARBOHYD 51 51
CC CARBOHYD 68 68
SQ SEQUENCE 137 AA; 14857 MW; 980BDE6F89A2E0BD CRC64;
Query Match 2.7%; Score 7; DB 1; Length 137;

Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 12 PPSLSS 18
Db 97 PPSLSS 103

RESULT 25
ID RSVR_COTUA STANDARD; PRT; 157 AA.
AC P98162;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Subgroup A Rous sarcoma virus receptors PG890 and PG950 precursor (Low density lipoprotein receptor-related protein).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Colurnix.
OC NCBI_TaxID=93934;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=9406516; PubMed=8402880;
RA Bates P., Young J.A., Varmus H.B.;
RT "A receptor for subgroup A Rous sarcoma virus is related to the low density lipoprotein receptor";
RL Cell 74:1043-1051(1993).
CC -1- FUNCTION: RESPONSIBLE FOR SUSCEPTIBILITY TO THE RETROVIRUS SUBGROUP A ROUS SARCOMA VIRUS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOPFORMS: PG900 (SHOWN HERE) AND PG850; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 1 LDL-RECEPTOR CLASS A DOMAIN.
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CC -----
DR EMBL; L22752; -; NOT_ANNOTATED_CDS.
DR EMBL; L22753; -; NOT_ANNOTATED_CDS.
DR HSSP; P01130; LLDL.
DR InterPro: IPR002172; LDL_recept_A.
DR Pfam: PF00057; ldl_recept_a.1.
DR SMART; SM00192; LDLA; 1.
DR PROSITE; PS01209; LDLRA_1; FALSE_NEG.
DR PROSITE; PS00068; LDLRA_2; 1.
KW Signal; Transmembrane; Alternative splicing; Receptor; Glycoprotein.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 157 ROUS SARCOMA VIRUS RECEPTOR PG900.
FT DOMAIN 20 102 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 103 125 POTENTIAL.
FT DOMAIN 126 157 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 71 LDL-RECEPTOR CLASS A.
FT DISULFID 30 47 BY SIMILARITY.
FT DISULFID 37 60 BY SIMILARITY.
FT DISULFID 54 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 24 24 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 81 81 VITICULAVG -> GIPCELYVMD (IN ISOPFORM PG850).
FT VARSPIC 110 120 MISSING (IN ISOPFORM PG850).
FT VARSPIC 121 157 MISSING (IN ISOPFORM PG850).
SQ SEQUENCE 157 AA; 16354 MW; 726B89AD96B7A66 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 107 LLLLPN 113
Db 10 LLLLPN 16

RESULT 26
ID COAE_RHIME STANDARD; PRT; 194 AA.
AC Q92TE9;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase).
GN COAE OR R00004 OR SMC02790.
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Rhizobiaceae; Sinorhizobium.
OC NCBI_TaxID=382;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J., Boistard P., Becker A., Boutry M., Cadieu E., Dreno S., Gloux S., Godie T., Goffeau A., Kahn D., Kles E., Lelaire V., Masny D., Pohl T., Portetelle D., Puelier A., Purnelle B., Ransberger U., Renard C., Thebaud P., Vandebol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -1- FUNCTION: Catalyzes the phosphorylation of the 3'-hydroxyl group of dephosphocoenzyme A to form coenzyme A (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP + dephospho-CoA = ADP + CoA.
CC -1- PATHWAY: Coenzyme A (CoA) biosynthesis: fifth (last) step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the coa family.
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CC -----
DR EMBL; AL591782; CAC41391.1; -;
DR InterPro: IPR001977; Depp_CoAkinase.
DR Pfam: PF01121; CoAE; 1.
DR PRODOM: PD003329; Depp_CoAkinase; 1.
DR TIGRfam; TIGR00152; UPR0038; 1.
DR PROSITE; PS01294; COAE; FALSE_NEG.
KW Transferrase; Kinase; ATP-binding; Coenzyme A biosynthesis; Complete proteome.
FT NP BIND 8 15 ATP (POTENTIAL).
SQ SEQUENCE 194 AA; 21336 MW; D26117AEAE81F69 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 29;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DE Cytochrome c oxidase polypeptide II (EC 1.9.3.1).
 GN COX2 OR COXII.
 OS Marchantia polymorpha (Liverwort).
 OC Mitochondrion.
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiophyta;
 CC Marchantiopsida; Marchantiales; Marchantiaceae; Marchantia.
 CC Marchantiaceae; Marchantia.
 OK NCBI_TaxId=3197;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92114051; PubMed=1731062;
 RA Oda K., Yamato K., Ohta E., Nakamura Y., Takemura M., Nozato N.,
 RA Akashi K., Kanegae T., Ogura Y., Kohchi T., Ohyama K.;
 RT "Gene organization deduced from the complete sequence of liverwort
 Marchantia polymorpha mitochondrial DNA. A primitive form of plant
 mitochondrial genome.";
 RL J. Mol. Biol. 223:1-7(1992).
 CC -1- FUNCTION: CYTOCHROME C OXIDASE IS THE COMPONENT OF THE RESPIRATORY
 CHAIN THAT CATALYZES THE REDUCTION OF OXYGEN TO WATER. SUBUNIT 1-
 CC 3 FORM THE FUNCTIONAL CORE OF THE ENZYME COMPLEX. SUBUNIT 2
 CC TRANSFERS THE ELECTRONS FROM CYTOCHROME C VIA ITS BINUCLEAR COPPER
 CC A CENTER TO THE BINUCLEAR CENTER OF THE CATALYTIC SUBUNIT 1.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- COFACTOR: Copper A.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE SUBUNIT 2 FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: M68929; AAC09432.1; -.
 CC DR PIR: S25950; S25950.
 CC DR InterPro: IPR001505; Copper_Cua.
 CC DR InterPro: IPR002429; Cyt_c-ox_2.
 CC DR Pfam: PF00116; COX2; 1.
 CC DR Pfam: PF02790; COX2_TM; 1.
 CC DR PRINTS: PR01166; CYCOXIDASEII.
 CC DR PRODOM: PD000131; Copper_Cua; 1.
 CC DR PROSITE: PS00078; COX2; 1.
 CC KW Oxidoreductase; Copper; Mitochondrion; Transmembrane; Inner membrane;
 CC Electron transport; Respiratory chain.
 CC FT DOMAIN 1 39 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
 CC FT TRANSMEM 40 60 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
 CC FT DOMAIN 61 75 MITOCHONDRIAL MATRIX (POTENTIAL).
 CC FT TRANSMEM 76 104 POTENTIAL.
 CC FT DOMAIN 105 251 MITOCHONDRIAL INTERMEMBRANE (POTENTIAL).
 CC FT METAL 184 184 COPPER A (PROBABLE).
 CC FT METAL 219 219 COPPER A (PROBABLE).
 CC FT METAL 223 223 COPPER A (PROBABLE).
 CC FT METAL 227 227 COPPER A (PROBABLE).
 CC SQ SEQUENCE 251 AA; 28693 MW; 1A6527DB503278A CRC64;
 Query Match 2.7%; Score 7; DB 1; Length 251;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Masticotoma protease precursor (EC 3.4.21.-).
 OS Canis familiaris (Dog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 CC NCBI_TaxId=9615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352460; PubMed=2504277;
 RA Vanderslice P., Craik C.S., Nadel J.A., Caughey G.H.;
 RT "Molecular cloning of dog mast cell tryptase and a related protease:
 RT structural evidence of a unique mode of serine protease activation.";
 RL Biochemistry 28:4148-4155(1989).
 CC -1- FUNCTION: MAST CELL TRYPTASE.
 CC -1- SIMILARITY: BELONGS TO TRYPTASE FAMILY S1.
 CC -----
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 CC -----
 CC DR EMBL: M24665; AAA30855.1; -.
 CC DR PIR: B32410; B32410.
 CC DR HSSP: P00763; IDPO.
 CC DR MEROPS: S01.145; -.
 CC DR InterPro: IPR001314; Chymotrypsin.
 CC DR InterPro: IPR001254; Ser_protease_Try.
 CC DR Pfam: PF00089; trypsin; 1.
 CC DR PRINTS: PR00722; CHYMOTRYPSIN.
 CC DR SMART: SM00020; TRYD_SPC; 1.
 CC DR PROSITE: PS00240; TRYPSIN_DOM; 1.
 CC DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 CC DR PROSITE: PS00135; TRYPSIN_SER; FALSE NEG.
 CC KW Hydrolyase; Serine protease; Signal; Glycoprotein.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 269 MASTOCYTOMA TRYPTASE.
 CC FT ACT SITE 66 66 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT SITE 116 116 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT ACT SITE 217 217 CHARGE RELAY SYSTEM (BY SIMILARITY).
 CC FT DISULFID 51 67 BY SIMILARITY.
 CC FT DISULFID 150 223 BY SIMILARITY.
 CC FT DISULFID 183 204 BY SIMILARITY.
 CC FT DISULFID 213 241 BY SIMILARITY.
 CC FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SQ SEQUENCE 269 AA; 29824 MW; B4MAAF7E4E2FD4E5 CRC64;
 Query Match 2.7%; Score 7; DB 1; Length 269;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 28
 TRYM_CANFA STANDARD; PRT; 269 AA.
 ID TRYM_CANFA
 AC P19236;
 DT 01-NOV-1990 (Rel. 16, Created)

OY 254 EAVSLDD 260
 |||||
 DB 235 EAVSLDD 241

RESULT 29
 ICE6_HUMAN STANDARD; PRT; 293 AA.
 ID ICE6_HUMAN
 AC P5512;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Caspase-6 precursor (EC 3.4.22.-) (Apoptotic protease Mch-2).
 GN CASP6 OR MCH2.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 CC NCBI_TaxId=9606;

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RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE-T-cell.
RX MEDLINE=95316841; PubMed=7796396.
RA Fernandez-Alnemri T., Litwack G., Alnemri E.S.;
RT "Mch2, a new member of the apoptotic Ced-3/Ice cysteine protease gene
RL family.";
RL Cancer Res. 55:2737-2742(1995).
RN [2]
RN PROCESSING.
RC TISSUE-Lymphocytes;
RX MEDLINE=97059171; PubMed=8900201;
RA Srinivasula S.M., Fernandes-Alnemri T., Zangirilli J., Robertson N.,
RA Armstrong R.C., Wang L., Trapani J.A., Tomaselli K.J., Litwack G.,
RA Alnemri E.S.;
RT "The Ced-3/interleukin 1beta converting enzyme-like homolog Mch2 and
RT the lamin-cleaving enzyme Mch2alpha are substrates for the apoptotic
RT mediator CPP32.";
RL J. Biol. Chem. 271:27099-27106(1996).
CC -1- FUNCTION: INVOLVED IN THE ACTIVATION CASCADE OF CASPASES
CC RESPONSIBLE FOR APOPTOSIS EXECUTION. CLEAVES POLY(ADP-RIBOSE)
CC POLYMERASE IN VITRO, AS WELL AS LAMINS. OVEREXPRESSION PROMOTES
CC PROGRAMMED CELL DEATH.
CC -1- SUBUNIT: HETERODIMER OF A 18 KDA (P18) AND A 11 KDA (P11) SUBUNIT.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; ALPHA (SHOWN HERE) AND BETA.
CC ARE PRODUCED BY ALTERNATIVE SPLICING. THE BETA ISOFORM DOES NOT
CC SEEM TO HAVE PROTEOLYTIC ACTIVITY.
CC -1- PTM: CLEAVAGES BY CPP32, CASPASE-8 OR -10 GENERATE THE TWO ACTIVE
CC SUBUNITS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C14.
CC
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CC -----
DR EMBL: U20536; AAC50168.1; -
DR EMBL: U20537; AAC50169.1; -
DR HSSP: P42574; 1PNU.
DR MEROPS: C14.005; -
DR Genew: HGNC:1507; CASP6.
DR MIM: 601532; -
DR InterPro: IPR002398; ICE.
DR InterPro: IPR002138; ICE_P10.
DR InterPro: IPR001309; ICE_P20.
DR Pfam: PF00655; ICE_P10; 1.
DR Pfam: PF00656; ICE_P20; 1.
DR PRINTS: PR00376; IL1BCEZYME.
DR SMART: SM00115; CASc; 1.
DR PROSITE: PS01122; CASPASE_CYS; 1.
DR PROSITE: PS01121; CASPASE_HIS; 1.
DR PROSITE: PS50207; CASPASE_P10; 1.
DR PROSITE: PS50208; CASPASE_P20; 1.
KW Hydrolyase; Thiol protease; Apoptosis; Zymogen; Alternative splicing.
FT PROPEP 1 23
FT CHAIN 24 179 CASPASE-6 SUBUNIT P18.
FT PROPEP 180 193
FT CHAIN 194 293 CASPASE-6 SUBUNIT P11.
FT ACT_SITE 121 121 BY SIMILARITY.
FT ACT_SITE 163 163 BY SIMILARITY.
FT VARSPIC 14 102 MISSING (IN ISOFORM BETA).
SQ SEQUENCE 293 AA; 33409 MW; BD9204E23CE1F670 CRC64;
Query Match 2.7%; Score 7; DB 1; Length 293;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
103 KAEELL 109
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DB 92 KAEELL 98
RESULT 30
RN_MOUSE STANDARD; PRT; 301 AA.
ID RN_MOUSE
AC 09CWB;
DT 15-JUN-2002 (rel. 41, Created)
DT 15-JUN-2002 (rel. 41, Last sequence update)
DE 15-JUN-2002 (rel. 41, Last annotation update)
DE Ribonuclease H1 large subunit (EC 3.1.26.-) (RNase H1 large subunit).
GN RNASEH2A OR RNASEH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Embryonic stem cells;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirral L.M., Stubbli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Guentrich S., Hill D., Hofmann M., Hume D.A., Kamaya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima U., Mazzarelli U., Nombetis P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlski S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RT Nature 409:685-690(2001).
CC -1- FUNCTION: Degrades the ribonucleotide moiety on RNA-DNA hybrid
CC MOLECULES. PARTICIPATES IN DNA REPLICATION (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
CC phosphomonoester.
CC -1- SIMILARITY: BELONGS TO THE RNASE H1 FAMILY. EUKARYOTIC
CC SUBFAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF010297; BAB26828.1; -
DR HSSP: Q57589; 1EKE.
DR WGD: MG1:1916974; 2400006P09RLK.
DR InterPro: IPR001352; RNase_H1/H11.
DR InterPro: IPR004649; Rnh11.
DR Pfam: PF01351; RNase_H1; 1.
DR TIGRFAMs: TIGR00729; Rnh11; 1.
KW Hydrolyase; Nuclease; Endonuclease.
FT ACT_SITE 34 34 BY SIMILARITY.
FT ACT_SITE 142 142 BY SIMILARITY.
FT ACT_SITE 170 170 BY SIMILARITY.
SQ SEQUENCE 301 AA; 33541 MW; A0F92D23F1DB43BF CRC64;
Query Match 2.7%; Score 7; DB 1; Length 301;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
187 LKPCVL 193

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Db 25 LKEPCVL 31

RESULT 31
OGG1_HUMAN STANDARD; PRT; 345 AA.
AC O15527; O00390; P78554; O00670; O00705; O14876; O95488; O9UL34;
AC O9Y6C4; O9Y6C4; O9UIK0; O9UIK1; O9UIK2; O9Y2C0; O9Y2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE N-glycosylase/DNA lyase [Includes: 8-oxoguanine DNA glycosylase
DE (EC 3.2.2.-); DNA (apurinic or apyrimidinic site) lyase
DE (EC 4.2.99.18) (AP lyase)].
GN OGG1 OR MMH OR MUTM OR OGH1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Colon;
RX MEDLINE=97330655; PubMed=9187114;
RA Aburatani H., Hippo Y., Ishida T., Takashima R., Matsuda C.,
RA Kodama T., Takao M., Yasui A., Yamamoto K., Asano M., Fukasawa K.,
RA Yoshinari T., Inoue H., Otsuka E., Nishimura S.;
RT "Cloning and characterization of mammalian 8-hydroxyguanine-specific
RT DNA glycosylase/apurinic, apyrimidinic lyase, a functional mutM
RT homologue.";
RL Cancer Res. 57:2151-2156(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=97352815; PubMed=9207108;
RA Rosenquist T.A., Zharkov D.O., Grollman A.P.;
RT "Cloning and characterization of a mammalian 8-oxoguanine DNA
RT glycosylase.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:7429-7434(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 2).
RX MEDLINE=97368311; PubMed=9223306;
RA Roldan-Arjona T., Wei Y.-F., Carter K.C., Klungland A., Anselmino C.,
RA Wang R.-P., Augustus M., Lindahl T.;
RT "Molecular cloning and functional expression of a human cDNA encoding
RT the antitumor enzyme 8-hydroxyguanine-DNA glycosylase.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:8016-8020(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=97368310; PubMed=9223305;
RA Radicella J.P., Dherin C., Desmaze C., Fox M.S., Boiteux S.;
RT "Cloning and characterization of hOGG1, a human homolog of the OGG1
RT gene of *Saccharomyces cerevisiae*.";
RL Proc. Natl. Acad. Sci. U.S.A. 94:8010-8015(1997).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=97342862; PubMed=9197244;
RA Lu R., Nash H.M., Verdine G.L.;
RT "A mammalian DNA repair enzyme that excises oxidatively damaged
RT guanine maps to a locus frequently lost in lung cancer.";
RL Curr. Biol. 7:397-407(1997).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=97334205; PubMed=9190902;
RA Arai K., Morishita K., Shimura K., Kohno T., Tanigaki M., Ohnada S.,
RA Yokota J.;
RT "Cloning of a human homolog of the yeast OGG1 gene that is involved in
RT the repair of oxidative DNA damage.";
RL Oncogene 14:2857-2861(1997).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=98012228; PubMed=9348312;
RA Kuo F.-C., Sklar J.L.;
RT "Augmented expression of a human gene for 8-oxoguanine DNA glycosylase

(mutM) in B lymphocytes of the dark zone in lymph node germinal
RT centers.";
RL J. Exp. Med. 186:1547-1556(1997).
RN [8]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RX MEDLINE=98026907; PubMed=9321410;
RA Bjoras M., Luna L., Johnsen B.E., Hoff E., Haug T., Rognes T.,
RA Seeberg E.;
RT "Opisome base-dependent reactions of a human base excision repair
RT enzyme on DNA containing 7,8-dihydro-8-oxoguanine and abasic sites.";
RL EMBO J. 16:6314-6322(1997).
RN [9]
RP SEQUENCE FROM N.A. (ISOFORM 1A).
RA Dhenant A., Boiteux S., Radicella J.;
RT "Genomic structure and promoter characterization of the human 8-OH-
RT guanine glycosylase gene (OGG1) gene.";
RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
RN [10]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99380087; PubMed=10449904;
RA Ishida T., Hippo Y., Nakahori Y., Matsushita I., Kodama T.,
RA Nishimura S., Aburatani H.;
RT "Structure and chromosome location of human OGG1.";
RL Cytogenet. Cell Genet. 85:232-236(1999).
RN [11]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE=99250157; PubMed=10233158;
RA Nishio K., Ohtsubo T., Oda H., Fujiwara T., Kang D., Sugimachi K.,
RA Nakabeppu Y.;
RT "Expression and differential intracellular localization of two major
RT forms of human 8-Oxoguanine DNA glycosylase encoded by alternatively
RT spliced OGG1 mRNAs.";
RL Mol. Biol. Cell 10:1637-1652(1999).
RN [12]
RP REVIEW.
RX MEDLINE=20239648; PubMed=10775435;
RA Boiteux S., Radicella J.P.;
RT "The human OGG1 gene: structure, functions, and its implication in the
RT process of carcinogenesis.";
RL Arch. Biochem. Biophys. 377:1-8(2000).
RN [13]
RP VARIANT HIS-154.
RX MEDLINE=98438755; PubMed=9765618;
RA Shimura K., Kohno T., Kasai H., Koda K., Sugimura H., Yokota J.;
RT "Infrequent mutations of the hOGG1 gene, that is involved in the
RT excision of 8-hydroxyguanine in damaged DNA, in human gastric
RT cancer.";
RL Jpn. J. Cancer Res. 89:825-828(1998).
RN [14]
RP VARIANT GLN-46.
RX MEDLINE=98324718; PubMed=9662341;
RA Chevillard S., Radicella J.P., Levalois C., Lebeau J., Poupon M.F.,
RA Oudard S., Dutrillaux B., Boiteux S.;
RT "Mutations in OGG1, a gene involved in the repair of oxidative DNA
RT damage, are found in human lung and kidney tumors.";
RL Oncogene 16:3083-3086(1998).
RN [15]
RP CHARACTERIZATION OF VARIANT CYS-326.
RX MEDLINE=99428653; PubMed=10497264;
RA Dherin C., Radicella J.P., Dizdaroğlu M., Boiteux S.;
RT "Excision of oxidatively damaged DNA bases by the human alpha-hOGG1
RT protein and the polymorphic alpha-hOGG1(ser326cys) protein which is
RT frequently found in human populations.";
RL Nucleic Acids Res. 27:4001-4007(1999).
RN [16]
RP CHARACTERIZATION OF VARIANTS GLN-46, HIS-154 AND CYS-326.
RX MEDLINE=20368626; PubMed=10908322;
RA Audebert M., Radicella J.P., Dizdaroğlu M.;
RT "Effect of single mutations in the OGG1 gene found in human tumors on
RT the substrate specificity of the ogg1 protein.";
RL Nucleic Acids Res. 28:2672-2678(2000).
CC -!- FUNCTION: DNA REPAIR ENZYME THAT INCISES DNA AT 8-OXOG RESIDUES.
EXCISES 7,8-DIHYDRO-8-OXOGUANINE AND 2,6-DIAMINO-4-HYDROXY-5-N-

| | | |
|----|--|--------------------------------|
| AC | 014318; | 30-MAY-2000 (Rel. 39, Created) |
| DT | 30-MAY-2000 (Rel. 39, | Last sequence update) |
| DT | 16-OCT-2001 (Rel. 40, | Last annotation update) |
| DE | 38 kDa FK-506 binding protein homolog (FKBP38) (FK506-binding protein 8). | |
| GN | FKBP8 OR FKBP38. | |
| OS | Homo sapiens (Human). | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. | |
| OX | NCBI_TaxId=9606; | |
| KX | (1) | |
| RX | SEQUENCE FROM N.A. MEDLINE=95369708; PubMed=7543869; Lam E., Martin M., Wiederrecht G.; Isolation of a cDNA encoding a novel human FK506-binding protein homolog containing leucine zipper and tetratricopeptide repeat motifs". Gene 160:297-302(1995). | |
| RL | (2) | |
| RP | SEQUENCE FROM N.A. Rutherford J.E., McCready P.M., Skowroneki E., Adamson A.W., Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stillwagen S., Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Dargman L., Poundstone P., Christensen M., Georgescu A., Ayila J., Lin S., Altix C., Andreise T., Tranheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan Q., Krommiller B., Krellano A., Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carraro A.V.; Sequence analysis of an 1 Mb region containing the MEFR2 gene in 19p12."; | |
| RL | Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases. | |
| CC | - FUNCTION: HAS NO PRPASE/ROTAASE ACTIVITY. | |
| CC | - SUBUNIT: HOMOMULTIMERS OR HETEROMULTIMERS (POTENTIAL). | |
| CC | - TISSUE SPECIFICITY: WIDELY EXPRESSED. HIGHEST LEVELS SEEN IN THE BRAIN. | |
| CC | - SIMILARITY: BELONGS TO THE FKBP-TYPE PRPASE FAMILY. | |
| CC | - SIMILARITY: CONTAINS 3 TPR REPEATS. | |
| CC | ----- | |
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| CC | ----- | |
| DR | EMBL; LJ7033; AAB00102.1; . | |
| DR | EMBL; AC005387; AAC28753.1; . | |
| DR | HSSP; P27124; 1ROT. | |
| DR | Genew; HGNC:3724; FKBP8. | |
| DR | MIM; 604840; . | |
| DR | InterPro; IPR001179; FKBP_PRIPase. | |
| DR | InterPro; IPR001440; TPR. | |
| DR | Pfam; PF00254; FKBP; 1. | |
| DR | Pfam; PF00515; TPR; 3. | |
| DR | PROSITE; PS00453; FKBP_PRIPASE_1; FALSE_NEG. | |
| DR | PROSITE; PS00454; FKBP_PRIPASE_2; FALSE_NEG. | |
| DR | PROSITE; PSS0059; FKBP_PRIPASE_3; 1. | |
| DR | TPR repeat, Repeat. | |
| FT | DOMAIN 63 147 PRIPASE, FKBP-TYPE. | |
| FT | REPEAT 167 200 TPR 1. | |
| FT | REPEAT 218 251 TPR 2. | |
| FT | REPEAT 252 285 TPR 3. | |
| SQ | SEQUENCE 355 AA; 38408 MW; 4D94DD8A52F246DBB CRC64; | |
| OY | Query Match 2.7%; Score 7; DB 1; Length 355; Best Local Similarity 100.0%; Pred. No. 50; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | |
| D5 | 35 ATAAAG 41 337 ATAAAG 343 | |

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RESULT 33
FKBP_MOUSE STANDARD; PRT; 355 AA.
ID FKBP_MOUSE
AC 035465;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 38 kDa FK-506 binding protein homolog (FKBP38) (FK506-binding protein
8) (mukBP38) OR SAM11.
GN FKBP8 OR FKBP38 OR SAM11.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxId=10090;
(1)
RN
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X DBA/2;
RX MEDLINE=99211287; PubMed=10197430;
RA Pedersen K.M., Finsen B., Cells U.B., Jensen N.A.;
RT "mufBP38: a novel murine immunophilin homolog differentially
expressed in Schwannoma cells and central nervous system neurons in
vivo."
RL Electrophoresis 20:249-255(1999).
CC -1- FUNCTION: HAS NO PHASE/ROTAMASE ACTIVITY (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FKBP-TYPE PHASE FAMILY.
CC -1- SIMILARITY: CONTAINS 3 TPR REPEATS.
-----
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-----
DR EMBL; AF030635; AA86422.1; -.
DR HSSP; P27124; IROT.
DR MGD; MG1:1341070; FKBP8.
DR InterPro; IPR001179; FKBP_PPIase.
DR InterPro; IPR001440; TPR.
DR Pfam; PF00254; FKBP; 1.
DR Pfam; PF00515; TPR; 2.
DR PROSITE; PS00453; FKBP_PPIASE_1; FALSE NEG.
DR PROSITE; PS00454; FKBP_PPIASE_2; FALSE NEG.
DR PROSITE; PS50059; FKBP_PPIASE_3; 1.
DR TPR repeat; Repeat.
KW DOMAIN
FT DOMAIN 63 147 PPIASE, FKBP-TYPE.
FT REPEAT 167 200 TPR 1.
FT REPEAT 218 251 TPR 2.
FT REPEAT 252 285 TPR 3.
SQ SEQUENCE 355 AA; 38614 MW; 3252DE061B0F3205 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 355;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OG Plasmid.
OC Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxId=1831;
(1)
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=95050323; PubMed=7961424;
RA Denome S.A., Oldfield C., Nash L.J., Young K.D.;
RT "Characterization of the desulfurization genes from Rhodococcus sp.
strain IGT58."
RL J. Bacteriol. 176:6707-6716(1994).
(2)
RN
RP SEQUENCE FROM N.A.
RX MEDLINE=96031556; PubMed=7574582;
RA Piddington C.S., Kovacevich B.R., Ramboeck J.;
RT "Sequence and molecular characterization of a DNA region encoding the
RT dibenzothiophene desulfurization operon of Rhodococcus sp. strain
RT IGT58."
RL Appl. Environ. Microbiol. 61:468-475(1995).
CC -1- FUNCTION: PART OF A PATHWAY TO REMOVE COVALENTLY BOUND SULFUR FROM
CC DIBENZOTHIOPHENE (DBT) WITHOUT BREAKING CARBON-CARBON BONDS. THIS
CC ENZYME METABOLIZES DBT-SULFONE (DBT02 OR DBT 5,5-DIOXIDE) TO 2-
CC HYDROXYBIPHENYL (2-HBP).
CC -1- CATALYTIC ACTIVITY: 2-(2-hydroxyphenyl)benzenesulfinate + H(2)O =
CC 2-hydroxybiphenyl + sulfite.
CC -1- COFACTOR: FMN (POTENTIAL).
CC -1- PATHWAY: SECOND STEP IN PATHWAY FROM DBT TO 2-HBP.
CC -1- SUBUNIT: HETERODIMER OF TWO SUBUNITS, SOXA AND SOXB.
CC -1- SIMILARITY: BELONGS TO THE NTA/SNAA/DSZA(SOXA) FAMILY OF
CC MONOOXYGENASES.
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-----
DR EMBL; U08850; AA56672.1; -.
DR HSSP; L37363; AA599483.1; -.
DR HYDROLase; Monooxygenase; Flavoprotein; FMN; Plasmid.
SQ SEQUENCE 365 AA; 39044 MW; DA6A86756DA23D6 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 365;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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RESULT 34
SOXB_RHOSO STANDARD; PRT; 365 AA.
ID SOXB_RHOSO
AC P54997;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Dibenzothiophene desulfurization enzyme B (EC 3.1.2.24).
GN SOXB OR DS2B.
OS Rhodococcus sp. (strain IGT58).

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RESULT 35
HMPA_VIBPA STANDARD; PRT; 394 AA.
ID HMPA_VIBPA
AC P40609;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Flavohemoprotein (Hemoglobin-like protein) (Flavohemoglobin).
GN HMP.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxId=670;
(1)
RN
RP SEQUENCE FROM N.A.
RC STRAIN=BB22;
RA McCarter L.L.;
RT Submitted (APR-1994) to the EMBL/Genbank/DBJ databases.
CC -1- DOMAIN: CONSISTS OF TWO DISTINCT DOMAINS; ONE IS A HEME-CONTAINING
CC OXYGEN BINDING DOMAIN IN THE N-TERMINAL REGION AND THE OTHER IS AN
CC FAD-CONTAINING REDUCTASE DOMAIN FOUND IN THE C-TERMINAL REGION.

```

-1- SIMILARITY: BELONGS TO THE GLOBIN FAMILY. TWO-DOMAIN FLAVOHEMOPROTEINS SUBFAMILY. -1- SIMILARITY: TO A NUMBER OF FAD/NAD(P) FLAVOPROTEIN OXIDOREDUCTASES.

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CC EMBL: U09005; AAA62130.1; -.
 DR HSSP: P04252; 1VHB.
 DR InterPro: IPR001834; Cyt B5 reductase.
 DR InterPro: IPR000971; Globin.
 DR InterPro: IPR001433; Oxid. FAD/NAD(P).
 DR Pfam: PF00042; Globin, 1.
 DR Pfam: PF00175; NAD binding, 1.
 DR Pfam: PF00970; FAD binding, 6; 1.
 DR PROSITE: PS01033; Globin, 1.
 KM Oxidoreductase; NADP; Heme; Flavoprotein; FAD; Iron transport;
 KW Oxygen transport; Transport.
 FT DOMAIN 1 136 GLOBIN.
 FT METAL 53 53 IRON (HEME DISTAL LIGAND)
 FT METAL 85 85 IRON (HEME PROXIMAL LIGAND)
 FT FT (BY SIMILARITY).
 FT NP BIND 268 273 NADP (RIBOSE PART) (BY SIMILARITY).
 SO SEQUENCE 394 AA; 44352 MW; 2AA8BA771C1A087E CRC64;

Query Match 2.7%; Score 7; DB 1; Length 394;
 Best Local Similarity 100.0%; Pred. No. 56;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 SLSSSVQ 21
 Db 207 SLSSSVQ 213

RESULT 36
 ZF38_HUMAN
 ID ZF38_HUMAN STANDARD; PRT; 473 AA.
 AC Q9Y5A6; Q9H0B5;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Zinc finger protein zfp-38 (NY-REN-21 antigen).
 GN ZFP38.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI Taxid=9606;
 RN [1] -
 RP SEQUENCE FROM N.A.
 RC TISSUE-Testis;
 RX MEDLINE=21154917; Pubmed=11230166;
 RA Wiemann S., Weill B., Wellenreuther R., Gassenhuber J., Glasl S.,
 RA Ansgorge W., Boecker M., Blocker H., Bauesachs S., Blum H.,
 RA Lauber J., Duesterhoeft A., Beyer A., Koerner K., Strack N.,
 RA Mewes H.-W., Ottenwaelder B., Obermaler B., Tampe J., Heubner D.,
 RA Wambutt R., Korn B., Klein M., Poustka A.;
 RT "Towards a catalog of human genes and proteins: sequencing and
 RT analysis of 500 novel complete protein coding human cDNAs";
 RL Genome Res. 11:422-435(2001).
 RP SEQUENCE OF 62-473 FROM N.A.
 RC TISSUE=Renal cell carcinoma;
 RX MEDLINE=99438124; Pubmed=10508479;
 RA Scanlan M.J., Gordon J.D., Williamson B., Stockert E., Bander N.H.,
 RA Jongeneel V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
 Old L.J.;

RT "Antigens recognized by autologous antibody in patients with renal-
 RT cell carcinoma";
 RU Int. J. Cancer 83:456-464(1999).
 CC -1- FUNCTION: STRONG TRANSCRIPTIONAL ACTIVATOR (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Nuclear (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 SCAN BOX.

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CC EMBL: AL136865; CAB66799.1; -.
 DR EMBL: AF151100; AAD42866.1; -.
 DR HSSP: P08153; 1ZPD.
 DR InterPro: IPR003309; Treg_SCAN.
 DR InterPro: IPR000822; Znf_C2H2.
 DR Pfam: PF00096; Zf_C2H2; 14.
 DR Pfam: PF02023; SCAN; 2.
 DR PRINTS: PR00048; ZINC_FINGER.
 DR Prodom: PD000003; Znf_C2H2; 7.
 DR SMART: SM00431; LER; 1.
 DR SMART: SM0355; ZNF_C2H2; 7.
 DR PROSITE: PS50804; SCAN_BOX; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE: PS50157; ZINC_FINGER_C2H2_2; 7.
 KM Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat;
 KW Transcription regulation; Activator.
 FT DOMAIN 45 127 SCAN_BOX.
 FT FT ZINC_FINGERS.
 FT ZN_FING 277 299 C2H2-TYPE.
 FT ZN_FING 305 327 C2H2-TYPE.
 FT ZN_FING 333 354 C2H2-TYPE.
 FT ZN_FING 360 382 C2H2-TYPE.
 FT ZN_FING 388 410 C2H2-TYPE.
 FT ZN_FING 416 438 C2H2-TYPE.
 FT ZN_FING 444 466 C2H2-TYPE.
 SO SEQUENCE 473 AA; 53658 MW; D9A26694B11AB96F CRC64;

Query Match 2.7%; Score 7; DB 1; Length 473;
 Best Local Similarity 100.0%; Pred. No. 66;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 IRRYRIH 151
 Db 376 IRRYRIH 382

RESULT 37
 HETW_ANASP
 ID HETW_ANASP STANDARD; PRT; 506 AA.
 AC P37693; Q44211;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Polyketide synthase hactm.
 GN HETW OR ALK5357.
 OS Anabaena sp. (Strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OK NCBI Taxid=103690;
 RN [1] -
 RP SEQUENCE FROM N.A.
 RC MEDLINE=94209228; Pubmed=8157596;
 RA Black T.A., Wolk C.P.;
 RT "Analysis of a Het- mutation in Anabaena sp. strain PCC 7120
 RT implicates a secondary metabolite in the regulation of heterocyst
 RT spacing";
 RL J. Bacteriol. 176:2282-2292(1994).

```

RN [2]
RN SEQUENCE FROM N.A.
RA Bauer C.C., Ramaswamy K.S., Endley S., Golden J.W., Haselkorn R.,
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=2159285; PubMed=11759840;
RA Kaneko T., Nakamura Y., Molk C.P., Kurita T., Saeamoto S.,
RA Watanabe A., Itiguchi M., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kohara M., Matsumoto M., Matsumoto A., Muraki A.,
RA Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
RA Yasuda M., Tabata S.;
RT "Complete genomic sequence of the filamentous nitrogen-fixing
RT cyanobacterium Anabaena sp. strain PCC 7120."
RL DNA Res. 8:205-213(2001).
CC -1- COFACTOR: CONTAINS 1 COVALENTLY BOUND PHOSPHOPANTHETHEINE (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 ACYL CARRIER DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L22883; AAA22001.1; -
DR EMBL; U04435; AAA03658.1; -
DR EMBL; AP003599; BAB7056.1; -
DR Interpro: IPR003880; Pantine_attach.
DR Pfam; PF00350; gp-binding; 1.
DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; FALSE_NEG.
DR PROSITE; PS50075; ACP_DOMAIN; 1.
KW Antibiotic biosynthesis; Oxidoreductase; Phosphopantetheine;
KW Multifunctional enzyme; Complete proteome.
FT DOMAIN 12 81 ACYL CARRIER (ACP).
FT BINDING 44 44 PHOSPHOPANTHETHEINE (BY SIMILARITY).
FT CONFLICT 442 442 F -> L (IN REF. 2).
SQ SEQUENCE 506 AA; 55766 MW; A3940C8E3A765588 CRC64;

Query Match
Best Local Similarity 2.7%; Score 7; DB 1; Length 506;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 116 GAFIRE 122
DB 147 GAFIRE 153

RESULT 38
YES_XIPHE STANDARD; PRT; 544 AA.
AC P27447;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Proto-oncogene tyrosine-protein kinase YES (EC 2.7.1.112) (P61-YES)
DE (C-YES).
DE GN YES.
OS Xiphophorus helleri.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorphi; Atherinomorpha;
OC Cyprinodontiformes; Poeciliidae; Xiphophorus.
OX NCBI_TaxID=8084;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Rio Lancelilla;
RX MEDLINE=91187435; PubMed=1707152;
RA Hannig G., Ottile S., Schachtl M.;
RT "Conservation of structure and expression of the c-yes and fyn genes
RT in lower vertebrates."

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RL Oncogene 6:361-369(1991).
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. SRC
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X54970; CA38714.1; -
DR HSP; P12931; IPWK.
DR Interpro: IPR000719; Bux_pkinase.
DR Interpro: IPR000980; SH2.
DR Interpro: IPR001452; SH3.
DR Interpro: IPR001245; Tyr_pkinase.
DR Pfam; PF00017; SH2; 1.
DR Pfam; PF00018; SH3; 1.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR000001; Bux_pkinase; 1.
DR ProDom; PD000066; SH3; 1.
DR ProDom; PD000093; SH2; 1.
DR SMART; SM00252; SH2; 1.
DR SMART; SM00326; SH3; 1.
DR SMART; SM00219; TyrcK; 1.
DR PROSITE; PS00107; TYRKINASE ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
KW Proto-oncogene; Tyrosine-protein kinase; Phosphorylation;
KW Transferrase; ATP-binding; Myristate; SH3 domain; SH2 domain.
FT LIPID 2 2 MYRISTATE (BY SIMILARITY).
FT DOMAIN 92 153 SH3.
FT DOMAIN 159 256 SH2.
FT NP_BIND 284 292 PROTEIN KINASE.
FT BINDING 284 292 ATP (BY SIMILARITY).
FT ACT_SITE 306 306 ATP (BY SIMILARITY).
FT MOD_RES 427 427 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE 544 AA; 61288 MW; 7D4181B3E7066F CRC64;

Query Match
Best Local Similarity 2.7%; Score 7; DB 1; Length 544;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 107 LLLPGN 113
DB 172 LLLPGN 178

RESULT 39
ZF38_MOUSE STANDARD; PRT; 555 AA.
AC Q07231;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Zinc finger protein 38 (Zfp-38) (CEP350) (Transcription factor RU49).
DE ZFP38 OR ZFP-38.
DE GN Mus musculus (Mouse).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

```

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BTBRTF; TISSUE=Spermatocyte;
 RX MEDLINE=93012481; PubMed=1397691;
 RA Noce T., Fujiwara Y., Sezaki M., Fujimoto H., Higashinakagawa T.;
 RT "Expression of a mouse zinc finger protein gene in both spermatocytes
 RT and oocytes during meiosis";
 RL Dev. Biol. 153:356-367(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6j
 RX MEDLINE=93183757; PubMed=1284028;
 RA Chowdhury K.;
 RT "The ubiquitous transactivator Zfp-38 is upregulated during
 RT spermatogenesis with differential transcription";
 RL Mech. Dev. 39:129-142(1992).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96189345; PubMed=8625807;
 RA Yang X.W., Zhong R., Heintz N.;
 RT "Granule cell specification in the developing mouse brain as defined
 RT by expression of the zinc finger transcription factor Rfx9";
 RL Development 122:555-566(1996).
 CC -1- FUNCTION: STRONG TRANSCRIPTIONAL ACTIVATOR. ASSOCIATED WITH
 CC MEIOSIS IN BOTH MALE AND FEMALE GAMETOGENESIS. MAY HAVE DIFFERENT
 CC FUNCTIONS IN SOMATIC CELLS.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN THE SPERMATOCYTES AND
 CC SPERMATIDS OF ADULT TESTES. IT IS ALSO PRESENT AT LOWER LEVELS IN
 CC THE OVARY, BRAIN, SPLEEN, EMBRYO AND FETUS.
 CC -1- DEVELOPMENTAL STAGE: FIRST DETECTED BETWEEN 2 AND 3 WEEKS AFTER
 CC BIRTH. IN PARALLEL WITH THE ONSET AND PROGRESSION OF MEIOSIS. IT
 CC IS EXPRESSED DURING OOGENESIS FROM THE PACHTENE STAGE OF MEIOTIC
 CC PROPHASE THROUGH TO POSTMEIOTIC CELLS.
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 SCAN BOX.
 CC -----
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 CC -----
 DR EMBL: D10630; BAA01480.1; -;
 DR EMBL: X63747; CA45280.1; -;
 DR EMBL: U41671; AAB03786.1; -;
 DR HSP: P08045; IZNF.
 DR MGD: MGI:99182; Zfp38.
 DR InterPro: IPR003309; Treg_SCAN.
 DR InterPro: IPR008222; Znf_C2H2.
 DR Pfam: PF00096; zf-C2H2; 7.
 DR Pfam: PF02023; SCAN; 1.
 DR PRINTS: PR00048; ZINCFINGER.
 DR PRODOM: PD000003; ZNF_C2H2; 6.
 DR SMART: SM00431; LERF_1.
 DR SMART: SM00355; ZNF_C2H2; 7.
 DR PROSITE: PS0804; SCAN_BOX; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 6.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 7.
 KW Zinc-finger; Metal-binding; DNA-binding; Nuclear protein; Repeat;
 KW Developmental protein; Spermatogenesis; Transcription regulation;
 KW Activator.
 FT DOMAIN 18 134 3 X 39 AA APPROXIMATE TANDEM REPEATS.
 FT REPEAT 18 36 1-1.
 FT REPEAT 57 95 1-2.
 FT REPEAT 96 134 1-3.
 FT DOMAIN 122 204 SCAN_BOX.
 FT DOMAIN 361 548 ZINC_FINGERS.
 FT ZN_FING 359 381 C2H2-TYPE.

FT ZN_FING 387 409 C2H2-TYPE.
 FT ZN_FING 415 436 C2H2-TYPE.
 FT ZN_FING 442 464 C2H2-TYPE.
 FT ZN_FING 470 492 C2H2-TYPE.
 FT ZN_FING 498 520 C2H2-TYPE.
 FT ZN_FING 526 548 C2H2-TYPE.
 FT ZN_FING 554 576 C2H2-TYPE.
 FT ZN_FING 593 615 C2H2-TYPE.
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 FT ZN_FING 14220 14242 C2H2-TYPE.
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 FT ZN_FING 16047 16069 C2H2-TYPE.
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 FT ZN_FING 16677 16699 C2H2-TYPE.
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 FT ZN_FING 16803 16825 C2H2-TYPE.
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 FT ZN_FING 17126 17148 C2H2-TYPE.
 FT ZN_FING 17189 17211 C2H2-TYPE.
 FT ZN_FING 17252 17274 C2H2-TYPE.
 FT ZN_FING 17315 17337 C2H2-TYPE.
 FT ZN_FING 17378 17400 C2H2-TYPE.
 FT ZN_FING 17441 17463 C2H2-TYPE.
 FT ZN_FING 17504 17526 C2H2-TYPE.
 FT ZN_FING 17567 17589 C2H2-TYPE.
 FT ZN_FING 17630 17652 C2H2-TYPE.
 FT ZN_FING 17693 17715 C2H2-TYPE.
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 FT ZN_FING 18890 18912 C2H2-TYPE.
 FT ZN_FING 18953 18975 C2H2-TYPE.
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 FT ZN_FING 19142 19164 C2H2-TYPE.
 FT ZN_FING 19205 19227 C2H2-TYPE.
 FT ZN_FING 19268 19290 C2H2-TYPE.
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 FT ZN_FING 20087 20109 C2H2-TYPE.
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 FT ZN_FING 20213 20235 C2H2-TYPE.
 FT ZN_FING 20276 20298 C2H2-TYPE.
 FT ZN_FING 20339 20361 C2H2-TYPE.
 FT ZN_FING 20402 20424 C2H2-TYPE.
 FT ZN_FING 20465 20487 C2H2-TYPE.
 FT ZN_FING 20528 20550 C2H2-TYPE.
 FT ZN_FING 20601 20623 C2H2-TYPE.
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 FT ZN_FING 21252 21274 C2H2-TYPE.
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 FT ZN_FING 21378 21400 C2H2-TYPE.
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 FT ZN_FING 21882 21904 C2H2-TYPE.
 FT ZN_FING 21945 21967 C2H2-TYPE.
 FT ZN_FING 22008 22030 C2H2-TYPE.
 FT ZN_FING 22071 22093 C2H2-TYPE.
 FT ZN_FING 22134 22156 C2H2-TYPE.
 FT ZN_FING 22197 22219 C2H2-TYPE.
 FT ZN_FING 22260 22282 C2H2-TYPE.
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 FT ZN_FING 22638 22660 C2H2-TYPE.
 FT ZN_FING 22701 22723 C2H2-TYPE.
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 FT ZN_FING 22827 22849 C2H2-TYPE.
 FT ZN_FING 22890 22912 C2H2-TYPE.
 FT ZN_FING 22953 22975 C2H2-TYPE.
 FT ZN_FING 23016 23038 C2H2-TYPE.
 FT ZN_FING 23079 23101 C2H2-TYPE.
 FT ZN_FING 23142 23164 C2H2-TYPE.
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 FT ZN_FING 23394 23416 C2H2-TYPE.
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 FT ZN_FING 23520 23542 C2H2-TYPE.
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 FT ZN_FING 23709 23731 C2H2-TYPE.
 FT ZN_FING 23772 23794 C2H2-TYPE.
 FT ZN_FING 23835 23857 C2H2-TYPE.
 FT ZN_FING 23898 23920 C2H2-TYPE.
 FT ZN_FING 23961 23983 C2H2-TYPE.
 FT ZN_FING 24024 24046 C2H2-TYPE.
 FT ZN_FING 24087 24109 C2H2-TYPE.
 FT ZN_FING 24150 24172 C2H2-TYPE.
 FT ZN_FING 24213 24235 C2H2-TYPE.
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 FT ZN_FING 24465 24487 C2H2-TYPE.
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 FT ZN_FING 24717 24739 C2H2-TYPE.
 FT ZN_FING 24780 24802 C2H2-TYPE.

DR InterPro: IP000014; PAS_domain.
 DR Pfam: PF00989; PAS: 1.
 DR SMART: SM00353; HLH: 1.
 DR SMART: SM0086; PAC: 1.
 DR SMART: SM0091; PAS: 2.
 DR PROSITE: PS00038; HLH_1: 1.
 DR PROSITE: PS0088; HLH_2: 1.
 DR PROSITE: PS50112; PAS: 1.
 DR Repeat: DNA-binding; Nuclear protein; Transcription regulation.
 KW DNA BIND 46 58
 FT DOMAIN 59 99
 FT DOMAIN 135 205
 FT DOMAIN 294 360
 FT DOMAIN 366 409
 FT DOMAIN 212 223
 SQ SEQUENCE 594 AA; 63736 MW; D6477696DF69A4B3 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 594;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 41
 ZF37_HUMAN STANDARD; PRT; 597 AA.
 AC Q9Y603;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Zinc finger protein Zfp-37.
 GN ZFP37.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RX MEDLINE=98252797; PubMed=9585434;
 RA Dreyer S.D., Zhou L., Machado M.A., Horton W.A., Zabel B.,
 RA Winterpacht A., Lee B.;
 RT Cloning, characterization, and chromosomal assignment of the human
 RT ortholog of murine Zfp-37, a candidate gene for Nager syndrome.";
 RL Mamm. Genome 9:458-462(1998).
 CC -1- FUNCTION: MAY BE INVOLVED IN TRANSCRIPTIONAL REGULATION.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT LOW LEVEL IN SEVERAL TISSUES
 CC INCLUDING FETAL HUMAN CARTILAGE.
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC -1- SIMILARITY: CONTAINS 1 KRAB DOMAIN.
 CC -----
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 CC or send an email to license@ebi.ac.uk).
 CC -----
 CC EMBL: AF022158; AAC8425.1; ALT_INIT.
 CC HSSP: P25490; IUBD.
 CC TRANSFAC: T04977;
 CC Genew: HGNC:12863; ZFP37.
 CC MIM: 602951;
 CC InterPro: IP0001909; KRAB.
 CC InterPro: IP000822; ZnF_C2H2.
 CC Pfam: PF00096; ZF-C2H2; 12.
 CC Pfam: PF01352; KRAB; 1.

DR PRINTS: PR00048; ZINC_FINGER.
 DR ProDom: PD000003; ZnF_C2H2; 11.
 DR SMART: SM00349; KRAB; 1.
 DR SMART: SM00355; ZnF_C2H2; 12.
 DR PROSITE: PS00805; KRAB: 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 11.
 DR PROSITE: PS0157; ZINC_FINGER_C2H2_2; 12.
 KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KW Nuclear protein; Repeat.

FT DOMAIN 1 70
 FT DOMAIN 260 590
 FT ZN_FING 260 282
 FT ZN_FING 288 310
 FT ZN_FING 316 334
 FT ZN_FING 344 366
 FT ZN_FING 372 394
 FT ZN_FING 400 422
 FT ZN_FING 428 450
 FT ZN_FING 456 478
 FT ZN_FING 484 506
 FT ZN_FING 512 534
 FT ZN_FING 540 562
 FT ZN_FING 568 590
 SQ SEQUENCE 597 AA; 67597 MW; 527B76119DFA446 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 597;
 Best Local Similarity 100.0%; Pred. No. 81;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SPSSSS 19
 DB 241 SPSSSS 247

RESULT 42
 RCK2_YEAST STANDARD; PRT; 610 AA.
 AC P38623; 002532; 006557;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Serine/threonine-protein kinase RCK2 (EC 2.7.1.1.-) (CAM kinase-like
 DE protein kinase CLK1).
 GN RCK2 OR CLK1 OR CMK3 OR YJR248W OR L6972.6.
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OS Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 ON NCBI_TaxID=4932;
 RX MEDLINE=94156178; PubMed=8112585;
 RA Dahlqvist A., Sunnerhagen P.;
 RT "Two novel deduced serine/threonine protein kinases from
 RT Saccharomyces cerevisiae.";
 RL Gene 139:27-33(1994).
 CC [2]
 CC SEQUENCE FROM N.A.
 CC STRAIN=AB320;
 CC STRAIN=YN 214;
 CC MEDLINE=97094707; PubMed=8939941;
 CC Melcher M.L., Thorner J.;
 RT "Identification and characterization of the CLK1 gene product, a
 RT novel Cam kinase-like protein kinase from the yeast Saccharomyces
 RT cerevisiae.";
 RL J. Biol. Chem. 271:29958-29966(1996).
 CC [3]
 CC SEQUENCE FROM N.A.
 CC STRAIN=5288C / AB972;
 CC Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 CC Favell A., Fulton L., Gattung S., Greco T., Kisten J.,
 CC Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jiler M.,
 CC Johnson D., Johnston L., Langston Y., Latreille P., Le T.,
 CC Mardis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,

RA Rikfen L., Riles L., Taich A., Trevasakis E., Vignati D.,
 RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
 RA Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- PM: AUTOPHOSPHORYLATED.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CAK SUBFAMILY.

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 CC or send an email to license@isb-sib.ch).

DR EMBL, X71065; CA50389.1; -
 DR EMBL, U23464; AAA64421.1; -
 DR EMBL, U20865; AAB67392.1; -
 DR PIR, S47901; S47901.
 DR HSP, 063450; 1A06.
 DR SGD, S0004238; RCK2.
 DR InterPro, IPR000719; Euk_pkinase.
 DR InterPro, IPR002290; Ser_thr_pkinase.
 DR Pfam, PF00069; pkinase; 1.
 DR ProDom, PD000001; Euk_pkinase; 1.
 DR SMART, SMO0220; S_TKC; 1.
 DR PROSITE, PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE, PS00108; PROTEIN KINASE ST; 1.
 DR PROSITE, PS50011; PROTEIN KINASE DOM; 1.
 KM Transferase; Serine/threonine-protein kinase; ATP-binding;
 KM Phosphorylation; Calmodulin-binding.
 FT DOMAIN 163 478 PROTEIN KINASE
 FT NP_BIND 169 177 ATP (BY SIMILARITY).
 FT BINDING 201 201 ATP (BY SIMILARITY).
 FT ACT_SITE 313 313 BY SIMILARITY.
 FT DOMAIN 493 506 CALMODULIN-BINDING (POTENTIAL).
 FT CONFLICT 109 109 N -> S (IN REF. 3).
 FT CONFLICT 188 188 H -> N (IN REF. 3).
 FT CONFLICT 233 233 A -> V (IN REF. 3).
 FT CONFLICT 328 328 P -> R (IN REF. 3).
 FT CONFLICT 456 456 S -> A (IN REF. 3).
 FT CONFLICT 569 610 DEQLQNNFQLTIDITITLQRRKKGQNDVGPITPISATIR
 E -> MNSMKICTSN (IN REF. 1).
 SQ SEQUENCE 610 AA; 68040 MW; DFE7B95E4D23A8A CRC64;

Query Match 2.7%; Score 7; DB 1; Length 610;
 Best Local Similarity 100.0%; Pred. No. 83;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 221 DSSLLFS 227
 Db 514 DSSLLFS 520

RESULT 43
 VC42_HAEN STANDARD; PRT; 631 AA.
 ID VC42_HAEN
 AC P44236;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Mu-like prophage Flumu protein gp42.
 GN H1514.
 OS Haemophilus influenzae.
 OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
 OC Haemophilus.
 OC NCBI_TaxID=727;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Rd / ATCC 51907;
 RX MEDLINE=95350630; PubMed=7542800;
 RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,

RA Kerlavage A.R., Bule C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
 RA McKemey K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
 RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
 RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
 RA Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
 RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
 RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
 RA Venter J.C.;
 RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
 RT Rd.";
 RL Science 269:496-512(1995).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: TO PHAGE MU PROTEIN GP42.

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DR EMBL, U12827; AAC23167.1; -
 DR TIGR, H1514; -
 KM Hypothetical protein; Transmembrane; Complete proteome.
 FT TRANSMEM 56 76 POTENTIAL.
 FT TRANSMEM 385 405 POTENTIAL.
 FT TRANSMEM 455 475 POTENTIAL.
 FT TRANSMEM 495 515 POTENTIAL.
 FT TRANSMEM 543 563 POTENTIAL.
 SQ SEQUENCE 631 AA; 66208 MW; 34E234C986406D82 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 631;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 168 SLQALVD 174
 Db 140 SLQALVD 146

RESULT 44
 PABP_SCHPO STANDARD; PRT; 653 AA.
 ID PABP_SCHPO
 AC P31209; P87135;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Polyadenylate-binding protein (Poly(A) binding protein) (PABP).
 GN PAB1 OR PABP OR SPAC57A7.04C.
 OS Schizosaccharomyces pombe (Fission Yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OC NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou J., Beat N., Hayes J., Baker S., Chillingworth T., Churcher C.M.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltham J., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harte J., Hiddleston J., Hodgson G.,
 RA Holtz S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagers K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovich E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volkart G., Weir R., Roben J., Gymnopoulos B.,
 RA Wellens I., Vanterre E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,
 RA Borzym K., Langer I., Beck A., Lehner H., Reihardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambach R., Punnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaune V., Motter S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rocher M., Gallard C., Talida V.A., Garzon A., Thode G.,
 RA Dominguez A., Revelle J., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Cerruti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of *Schizosaccharomyces pombe*."
 RL Nature 415:871-880(2002).
 RN [2]
 RP SEQUENCE OF 15-628 FROM N.A.
 RX MEDLINE=91260690; PubMed=1575426.
 RA Burd C.G., Matunis E.L., Deylunas G.,
 RT "The multiple RNA-binding domains of the mRNA poly(A)-binding protein
 have different RNA-binding activities.";
 RL Mol. Cell. Biol. 11:3419-3424(1991).
 CC -1- FUNCTION: BINDS THE POLY(A) TAIL OF MRNA.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: CONTAINS 4 RNA RECOGNITION MOTIFS (RRM).
 CC -----
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 CC -----
 DR EMBL: Z95396; CAB08762.1; -;
 DR EMBL: M64603; AAA53520.1; -;
 DR PIR: A39720; DNZPPA.
 DR HSSP: P11940; ICVJ.
 DR InterPro: IPR002004; PABP/HECT.
 DR InterPro: IPR000504; RNA_rec_mot.
 DR Pfam: PF00076; rrm; 4.
 DR Pfam: PF00658; PABP; 1.
 DR SMART: SM00517; PolyA; 1.
 DR SMART: SM00360; RRM; 4.
 DR PROSITE: PS00102; RRM; 4.
 DR PROSITE: PS00030; RRM_RNP_1; 3.
 KW RNA-binding; Repeat.
 FT DOMAIN 80 158 RNA-BINDING (RRM) 1.
 FT DOMAIN 168 245 RNA-BINDING (RRM) 2.
 FT DOMAIN 261 338 RNA-BINDING (RRM) 3.
 FT DOMAIN 364 441 RNA-BINDING (RRM) 4.
 FT CONFLICT 15 34 ESDVTNNNEAVSESTKRESS -> MSLENSSTLSLCSNNT
 FT CONFLICT 349 349 THFW (IN REF. 2).
 FT CONFLICT 518 526 R -> A (IN REF. 2).
 FT CONFLICT 518 526 TOPPAGGA -> PLUSLEVR (IN REF. 2).
 SQ SEQUENCE 653 AA; 768F5CADD9DCFE1 CRC64;
 Query Match 2.7%; Score 7; DB 1; Length 653;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 43 PPAAGGA 49
 DB 520 PPAAGGA 526
 RESULT 45
 SPEI ARATH STANDARD; PRT; 702 AA.
 ID SPEI ARATH
 AC 095164; Q38938;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Arginine decarboxylase 1 (EC 4.1.1.19) (ARGDC 1) (ADC 1) (ADC-O).
 GN SPEI OR AT2G16500 OR FLP15.12.
 OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustroids II; Brassicales; Brassicaceae; Arabidopsi.
 OK NCBI_taxonomy:3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=96347400; PubMed=8756495;
 RA Watson M.B., Walenberg R.L.,
 RT "Regulation of Arabidopsis thaliana (L.) Heyn Arginine decarboxylase
 by potassium deficiency stress.";
 RL Plant Physiol. 111:1077-1083(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-T., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldlynn T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.U., Rensing C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen W., Pei G., Van Aken S., Umeyam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Coppenhaver G.P., Preuss D.,
 RA Nielsen W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.,
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 thaliana.";
 RL Nature 402:761-768(1999).
 CC -1- CARBOXYLIC ACTIVITY: L-arginine = aspartate + CO(2).
 CC -1- COPFACTOR: PYRIDOXAL PHOSPHATE AND MAGNESIUM.
 CC -1- PATHWAY: FIRST STEP IN ONE OF THE TWO PUTRESCINE SYNTHESIS
 PATHWAYS IN PLANTS.
 CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGinine
 DECARBOXYLASES.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U52851; AAB09723.1; -;
 DR EMBL: AC007195; AAD6494.1; -;
 DR InterPro: IPR000183; Decarboxylase2.
 DR Pfam: PF00278; Orn_Arg_dec_1.
 DR Pfam: PF02784; Orn_Arg_dec_N; 1.
 DR PRINTS: PR01179; ODADCBXBLASE.
 DR TIGRfam: TIGR01273; spea; 1.
 DR PROSITE: PS00878; ODR_DC_2; 1.
 DR PROSITE: PS00879; ODR_DC_2; 1.
 KW Pyridoxal phosphate; Decarboxylase
 KW Pyridoxal phosphate; Decarboxylase
 FT DOMAIN 320 330 SUBSTRATE-BINDING (BY SIMILARITY).
 FT CONFLICT 452 452 S -> F (IN REF. 1).
 FT CONFLICT 452 452 S -> F (IN REF. 1).
 SQ SEQUENCE 702 AA; 8B9D182B284BCA0 CRC64;
 Query Match 2.7%; Score 7; DB 1; Length 702;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 13 SPGLSSS 19
 DB 35 SPGLSSS 41
 RESULT 46
 SPEI BRAUT STANDARD; PRT; 702 AA.
 ID SPEI BRAUT
 AC 082475;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Arginine decarboxylase 1 (EC 4.1.1.19) (ARGDC 1) (ADC 1) (ADC-O).
 GN SPEI OR AT2G16500 OR FLP15.12.
 OS Arabidopsis thaliana (Mouse-ear cress).

```

DE Arginine decarboxylase (EC 4.1.1.19) (ARGDC) (ADC).
GN ADCL.
OS Brassica juncea (leaf mustard) (Indian mustard).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3707;
RN [1]
RP SEQUENCE FROM N.A.
RA Mo H., Pua E.-C.;
RT "Molecular cloning of an arginine decarboxylase cDNA from mustard
RT (Brassica juncea [L.] Czern & Coss)."
RL (In) Plant Gene Register FGR98-160.
CC -1- CATALYTIC ACTIVITY: L-arginine = agmatine + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE AND MAGNESIUM.
CC -1- PATHWAY: FIRST STEP IN ONE OF THE TWO PUTRESCINE SYNTHESIS
CC PATHWAYS IN PLANTS.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE
CC DECARBOXYLASES.
CC -----
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CC -----
DR EMBL; AF077547; AAC62017.1;
DR InterPro; IPR000183; Decarboxylase2.
DR Pfam; PF00278; Orn_DAP_Arg_dec; 1.
DR Pfam; PF02784; Orn_Arg_dec_N; 1.
DR PRINTS; PR01179; ODACRBLXASE.
DR TIGRFAMs; TIGR01273; spea; 1.
DR PROSITE; PS00878; ODR_DC_2_2; 1.
DR PROSITE; PS00879; ODR_DC_2_2; 1.
DR Putrescine biosynthesis; Spermidine biosynthesis; Lyase; Magnesium;
DR Pyridoxal phosphate; Decarboxylase.
DR DOMAIN 325 335 SUBSTRATE-BINDING (BY SIMILARITY).
DR PT DOMAIN 325 335
SQ SEQUENCE 702 AA; 76187 MW; 4FF2C7A801B1B92 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 702;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SPSSLS 19
Db 37 SPSSLS 43

RESULT 47
SPEC_ARATH STANDARD; PRT; 711 AA.
ID SPEC_ARATH
AC 023141;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 16-OCT-2001 (Rel. 40; Last annotation update)
DE Arginine decarboxylase 2 (EC 4.1.1.19) (ARGDC 2) (ADC 2) (ADC-N).
GN SPEC_ARATH AT4G34710 OR TA220.290.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Watson M.B., Yu W., Galloway G., Malmberg R.L.;
RT "Isolation and characterization of a second arginine decarboxylase
RT cDNA from Arabidopsis.",
RL (In) Plant Gene Register PGR97-114.
RN [2]
RP SEQUENCE FROM N.A.

RC STRAIN=cv. Columbia;
RX MEDLINE=20083488; PubMed=10617198;
RA Mayer K.F.X., Schueller C., Mambour R., Murphy G., Volckaert G.,
RA Pohl T., Duesterhoeft A., Striekema W., Entian K.-D., Terryn N.,
RA Harris B., Ansoorge W., Brandt P., Grivell L.A., Rieger M.,
RA Weisbeeggartner M., de Simone V., Obermair B., Maehre R., Mueller M.,
RA Kreis M., Deleney M., Puigdomenech P., Watson M., Schmidtmann T.,
RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
RA Vos P., Hohnel J., Zimmermann W., Wedler H., Ridley P.,
RA Langham S.-A., McCullagh B., Billham L., Robben J.,
RA Van der Schueren J., Grymonprez B., Chang Y.-J., Vandenbussche F.,
RA Breken M., Welfens I., Voet M., Bastiaens I., Aert R., Defoor E.,
RA Weitzengraber T., Boche G., Ramepeter U., Hilbert H., Braum M.,
RA Holzner E., Brandt A., Peters S., Van Staeren M., Dirse W.,
RA Moolman P., Klein Lankhorst R., Rose W., Hauf U., Koeller P.,
RA Beneser S., Hempel S., Feldpausch M., Lambrecht S., Van den Daele H.,
RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
RA Clark L., Doggett J., Hall S., Kay W., Lennard N., McIlroy K.,
RA Petret A., Rajandream M.A., Lyne M., Bense V., Rechmann S.,
RA Botkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
RA Dose S., de Haan W., Maatse A.C., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fartmann B., Grandenath K., Dauner D., Herzi A.,
RA Neumann S., Agirion A., Vitale D., Liqiori R., Piravandi E.,
RA Maessen O., Quigley F., Clabaud G., Muendlein A., Felber R.,
RA Schnabel S., Hiller R., Schmidt W., Lechery A., Aubourg S.,
RA Chefdor F., Cooke R., Berger C., Montfort A., Casachabeta E.,
RA Gibbons T., Weber N., Vandenbol M., Barques M., Terol J., Torres A.,
RA Perez-Perez A., Fumelle B., Bent E., Johnson S., Tacon D., Jesse T.,
RA Heijman L., Schwarz S., Scholler P., Heber S., Francis P., Biele C.,
RA Frishman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
RA Zaccaria P., Bevan M., Wilson R.K., de la Baitelle E., Spiegler K.,
RA Parnell L., Dedhia N., Gnoj L., Schutz K., Huang E., Hagermann K.,
RA Sekhon M., Murray J., Sheel P., Cordes M., Abu-Thaidh J.,
RA Stoneking T., Kalicki J., Graves T., Hamon G., Edwards J.,
RA Lattelle P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
RA Mix P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
RA Kimer P., Fulton L., Maris E., Danne M., Pegin K., Hiller L.,
RA Nelson J., Spieth J., Ryan E., Andrews S., Giesel C., Layman D.,
RA Du H., Ali J., Bergthoff A., Jones K., Dione K., Cotton M., Joshi C.,
RA Antoniou B., Zidanic M., Strong C., Sun H., Lamar B., Jordan C.,
RA Ma P., Zhong Z., Preston R., Vill D., Shekhar M., Matero A., Shah R.,
RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Tili S.,
RA Granel S., Shohdy N., Haasegawa A., Hamed A., Lodi M., Johnson A.,
RA Chen B., Maria W., Martensen R., McCombie W.R.;
RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
RT thaliana."
RL Nature 402:769-777(1999).
CC -1- CATALYTIC ACTIVITY: L-arginine = agmatine + CO(2).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE AND MAGNESIUM.
CC -1- PATHWAY: FIRST STEP IN ONE OF THE TWO PUTRESCINE SYNTHESIS
CC PATHWAYS IN PLANTS.
CC -1- SIMILARITY: BELONGS TO FAMILY 2 OF ORNITHINE, DAP, AND ARGININE
CC DECARBOXYLASES.
CC -----
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CC -----
DR EMBL; AF009647; AAB72179.1;
DR EMBL; AL023094; CA18850.1;
DR EMBL; AL161586; CAB80188.1;
DR InterPro; IPR000183; Decarboxylase2.
DR Pfam; PF00278; Orn_DAP_Arg_dec; 1.
DR Pfam; PF02784; Orn_Arg_dec_N; 1.
DR PRINTS; PR01179; ODACRBLXASE.
DR TIGRFAMs; TIGR01273; spea; 1.
DR PROSITE; PS00878; ODR_DC_2_1; 1.
DR PROSITE; PS00879; ODR_DC_2_2; 1.

```

KM Putrescine biosynthesis; Spermidine biosynthesis; Lyase; Magnesium;
 KM Pyridoxal phosphate; Decarboxylase.
 FT DOMAIN 331 SUBSTRATE-BINDING (BY SIMILARITY).
 SQ SEQUENCE 711 AA; 77219 MW; 88003877173DEES CRC64;

Query Match 2.7%; Score 7; DB 1; Length 711;
 Best Local Similarity 100.0%; Pred. No. 96;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 SPSSSS 19
 Db 43 SPSSSS 49

RESULT 48
 ID 2267_HUMAN STANDARD; PRT; 743 AA.

AC Q14586; Q9NRJ0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Zinc finger protein 267 (Zinc finger protein HZF2).
 GN ZNF267.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]

RP SEQUENCE FROM N.A.
 RA Schaefer U., Schneider A., Neugebauer E.;
 RT "Identification of a nitric oxide regulated krueppel-like zinc finger
 RT protein using motif directed differential display";
 RN Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 [2]

RP SEQUENCE OF 12-743 FROM N.A.
 RX MEDLINE=95169271; PubMed=7865130;
 RA Adlink M., Aveskogh M., Hellman L.;
 RT "Isolation of cDNA clones for 42 different Krueppel-related zinc finger
 RT proteins expressed in the human monoblast cell line U-937";
 RL DNA Cell Biol. 14:125-136(1995).
 CC -1- FUNCTION: MAY FUNCTION AS A TRANSCRIPTION FACTOR.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.

CC -1- SIMILARITY: CONTAINS 1 KRAA DOMAIN.

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CC EMBL: AF220492; AF73867.1; -;
 DR EMBL: X78925; CA55525.1; -;
 DR HSSP: P07248; IARF.
 DR Genew: HGNC:13060; ZNF267.
 DR MIM: 604752; -;
 DR InterPro: IPR001909; KRAA.
 DR InterPro: IPR000822; ZnfC2H2.
 DR Pfam: PF00096; zf-C2H2; 30.
 DR Pfam: PF01352; KRAA; 2.
 DR ProDom: PD000003; ZnfC2H2; 10.
 DR SMART: SM00349; KRAA; 1.
 DR SMART: SM00355; ZnfC2H2; 15.
 DR PROSITE: PS50805; KRAA; 1.
 DR PROSITE: PS00028; ZINC_FINGER_C2H2_1; 14.
 DR PROSITE: PS00157; ZINC_FINGER_C2H2_2; 14.
 KM Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
 KM Nuclear protein; Repeat.
 FT DOMAIN 4 75 KRAA
 FT DOMAIN 267 738 ZINC_FINGERS.

FT ZN_FING 267 289 C2H2-TYPE.
 FT ZN_FING 322 340 C2H2-TYPE (ATYPICAL).
 FT ZN_FING 380 402 C2H2-TYPE.
 FT ZN_FING 408 430 C2H2-TYPE.
 FT ZN_FING 436 458 C2H2-TYPE.
 FT ZN_FING 464 486 C2H2-TYPE.
 FT ZN_FING 492 514 C2H2-TYPE.
 FT ZN_FING 520 542 C2H2-TYPE.
 FT ZN_FING 548 570 C2H2-TYPE.
 FT ZN_FING 576 598 C2H2-TYPE.
 FT ZN_FING 604 626 C2H2-TYPE.
 FT ZN_FING 632 654 C2H2-TYPE.
 FT ZN_FING 660 682 C2H2-TYPE.
 FT ZN_FING 688 710 C2H2-TYPE.
 FT ZN_FING 716 738 C2H2-TYPE.
 SQ SEQUENCE 743 AA; 87447 MW; 35C69933E375B4C0 CRC64;

Query Match 2.7%; Score 7; DB 1; Length 743;
 Best Local Similarity 100.0%; Pred. No. 1e+02;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 145 IHRYRH 151
 Db 564 IHRYRH 570

RESULT 49

ID TPB6_YEAST STANDARD; PRT; 754 AA.

AC P40328; P40324; Q02845; Q05773;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Probable 26S protease subunit YTA6 (TAT-binding homolog 6).
 GN YTA6 OR YPL074W OR LPE11C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_Taxid=4932;
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c;
 RX MEDLINE=95274317; PubMed=7754704;
 RA Schnall R., Mannhaupt G., Stucka R., Tauer R., Ehle S.,
 RA Scharflose C., Vetter I., Feldmann H.,
 RT "Identification of a set of yeast genes coding for a novel family of
 RT putative ATPases with high similarity to constituents of the 26S
 RT protease complex";
 RL Yeast 10:1141-1155(1994).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=S288c / AB972;
 RX MEDLINE=97333271; PubMed=9169875;
 RA Bussey H., Storms R.K., Ahmed A., Alberman K., Allen E., Ansgore W.,
 RA Arayo R., Aparicio A., Bartell B.G., Badcock K., Bene V.,
 RA Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
 RA Chung E., Churcher C.M., Coster F., Davis R., Davis R.W.,
 RA Dietrich F.S., Delius H., DiPaolo T., Dubois E., Duesterhoef A.,
 RA Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
 RA Hall J., Hebling U., Heumann K., Hillbert H., Hillier L.,
 RA Hunnicke-Smith S., Hyman R., Johnston M., Kaiman S., Kleine K.,
 RA Komp C., Kuri O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
 RA Marthe R., Messenguy F., Mews H.-W., Mitsuhashi S., Moestl D.,
 RA Mueller-Auer S., Namath A., Nentwich U., Oeffner P., Pearson D.,
 RA Petel F.X., Pohl T.M., Purnelle D., Schaefer M., Scharfe M.,
 RA Scherrens B., Schramm S., Schroeder M., Sdicu A.M., Tetteelin H.,
 RA Uristarazu L.A., Ushinsky S., Vierendeels F., Visers S., Vose H.,
 RA Walsh S.V., Wambut R., Wang Y., Wedler E., Wedler H., Winnett E.,
 RA Zhong W.W., Zollner A., Vo D.H., Hani J.,
 RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI";
 RL Nature 387:103-105(1997).
 RN [3]

```

RX MEDLINE=87089718; PubMed=3025612;
RA Baker H.V.;
RT "Glycolytic gene expression in Saccharomyces cerevisiae: nucleotide
RL sequence of GCR1, null mutants, and evidence for expression.";
RL Mol. Cell. Biol. 6:3774-3784(1996).
CC -1- SIMILARITY: BELONGS TO THE AAA FAMILY OF ATPASES.
CC -1- CAUTION: Ref.1 sequence differs from that shown due to a number of
CC sequencing errors that include frameshifts and rearrangements.
CC -----
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CC -----
DR EMBL; X81071; CAA56960.1; ALT_FRAME.
DR EMBL; X81071; CAA56959.1; ALT_FRAME.
DR EMBL; U41849; AAB68264.1; -.
DR EMBL; M14145; AAB6912.1; -.
DR PIR; S6113; S6113.
DR SGD; S0005995; YTA6.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003959; AAA_ATPase_cent.
DR InterPro; IPR003960; AAA_sub.
DR Pfam; PF00004; AAA_1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00674; AAA; 1.
DR ATP-binding.
FT NP_BIND 511 518 ATP (POTENTIAL).
FT CONFLICT 20 20 L -> LQL (IN REF. 3).
FT CONFLICT 85 85 D -> I (IN REF. 3).
SQ SEQUENCE 754 AA; 85299 MW; 709F33D56382356 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SPSSSS 19
Db 120 SPSSSS 126

RESULT 50
ID OCT1_XENLA STANDARD; PRT; 760 AA.
AC P16143;
DT 01-APR-1990 (Rel. 14. Created)
DT 01-AUG-1991 (Rel. 19. Last sequence update)
DT 15-JUN-2002 (Rel. 41. Last annotation update)
DE Octamer-binding transcription factor 1 (OTF-1) (NF-A1) (XOCT1).
GN OCT1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90221827; PubMed=2326173;
RA Smith D.P.; Old R.W.;
RT "Nucleotide sequence of Xenopus laevis Oct-1 cDNA.";
RL Nucleic Acids Res. 18:369-369(1990).
RN [2]
RP SEQUENCE OF 261-335 FROM N.A.
RA Schluthuis U.G.; Baatends W.M.; Peterson-Maduro J.; Destré O.H.J.;
RL Submitted (FEB-1990) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN IS A TRANSCRIPTION FACTOR FOR SMALL NUCLEAR
CC RNA AND HISTONE H2B GENES.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: BELONGS TO THE POU TRANSCRIPTION FACTOR FAMILY.
CC CLASS-2 SUBFAMILY.

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CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.
CC -----
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CC -----
DR EMBL; X17190; CAA35051.1; -.
DR EMBL; X51819; CAA36119.1; ALT_INIT.
DR PIR; S07896; S07896.
DR HSSP; P14859; 1OCT.
DR TRANSPAC; T00642; -.
DR InterPro; IPR001356; Homeobox.
DR InterPro; IPR00972; Octamer-bind_TF.
DR InterPro; IPR000227; POU_domain.
DR Pfam; PF00046; homeobox; 1.
DR Pfam; PF00157; pou; 1.
DR PRINTS; PR00029; OCTAMER.
DR PRINTS; PR00028; POUDOMAIN.
DR ProDom; PD000010; Homeobox; 1.
DR ProDom; PD000583; POU domain; 1.
DR SMART; SM00389; HOX; 1.
DR SMART; SM00352; POU; 1.
DR PROSITE; PS00027; HOMEBOX_1; 1.
DR PROSITE; PS00035; POU_1; 1.
DR PROSITE; PS00465; POU_2; 1.
DR PROSITE; PS50071; HOMEBOX_2; 1.
KW Homeobox; DNA-binding; Transcription regulation; Activator;
KW Nuclear protein.
FT DNA_BIND 298 368 POU.
FT DNA_BIND 397 456 HOMEBOX.
SQ SEQUENCE 760 AA; 79097 MW; 706369DA9018345 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 SPSSSS 19
Db 540 SPSSSS 546

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Search completed: March 24, 2003, 16:07:23
Job time : 21 secs

